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(54) Title: NOVEL COMPOUNDS

(57) Abstract

This invention relates to newly identified polynucleotides, polypeptides encoded by such polynucleotides, the uses of such polynucleotides and polypeptides, as well as the production of such polynucleotides and polypeptides and recombinant host cells transformed with the polynucleotides. This invention also relates to inhibiting the biosynthesis or action of such polynucleotides or polypeptides and to the use of such inhibitors in therapy.

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NOVEL COMPOUNDS

Field of the Invention:

This invention relates to newly identified polynucleotides, polypeptides encoded by such polynucleotides, the uses of such polynucleotides and polypeptides, as well as the production of such polynucleotides and polypeptides and recombinant host cells transformed with the polynucleotides. This invention also relates to inhibiting the biosynthesis or action of such polynucleotides or polypeptides and to the use of such inhibitors in therapy. Preferred embodiments of the invention include Streptococcal polypeptides and polynucleotides, particularly those of *Streptococcus pneumoniae*.

Background of the Invention:

The Streptococci make up a medically important genera of microbes known to cause several types of disease in humans, including otitis media, pneumonia and meningitis. Since its isolation more than 100 years ago, *Streptococcus pneumoniae* has been one of the more intensively studied microbes. For example, much of our early understanding that DNA is, in fact, the genetic material was predicated on the work of Griffith and of Avery, Macleod and McCarty using this microbe. Despite the vast amount of research with *S. pneumoniae*, many questions concerning the virulence of this microbe remain.

While certain Streptococcal factors associated with pathogenicity have been identified, e.g., capsule polysaccharides, peptidoglycans, pneumolysins, PspA Complement factor H binding component, autolysin, neuraminidase, peptide permeases, hydrogen peroxide, IgA1 protease, the list is certainly not complete. Further very little is known concerning the temporal expression of such genes during infection and disease progression in a mammalian host. Discovering the sets of genes the bacterium is likely to be expressing at the different stages of infection, particularly when an infection is established, provides critical information for the screening and characterization of novel antibacterials which can interrupt pathogenesis. In addition to providing a fuller understanding of known proteins, such an approach will identify previously unrecognised targets.

Brief Description of the Invention:

This invention provides novel proteins, particularly those from *Streptococcus pneumoniae*, strain 0100993, characterised in that it comprises the amino acid sequences given herein or fragments, analogues or derivatives thereof.

In accordance with another aspect of the present invention, there are provided polynucleotides (DNA or RNA) which encode such polypeptides.

In particular the invention provides polynucleotides having the DNA sequences given herein.

The invention also relates to novel oligonucleotides derived from the sequences given herein which can act as PCR primers in the process herein described to determine whether or not the *Streptococcus pneumoniae* gene identified herein in whole or in part is expressed in infected tissue. It is recognised that such sequences will also have utility in diagnosis of the stage of infection and type of infection the pathogen has attained. The proteins so identified are also useful as targets in screens designed to identify antimicrobial compounds.

It is an object of the invention to provide polypeptides that have been identified as novel polypeptides by homology between the amino acid sequence set out in the Sequence Listing and a known amino acid sequence or sequences of other proteins such as the proteins identified under the heading Identity in Table 1.

It is a further object of the invention to provide polynucleotides that encode polypeptides set forth in the Sequence Listing, particularly polynucleotides that encode the polypeptide set forth in the Sequence Listing.

In a particularly preferred embodiment of the invention the polynucleotide comprises a region encoding polypeptides comprising the sequence set out in the Sequence Listing, or a variant thereof.

In another particularly preferred embodiment of the invention there is a novel protein from comprising an amino acid sequence of the Sequence Listing, or a variant thereof.

In accordance with another aspect of the invention, there is provided the use of a polynucleotide of the invention for therapeutic or prophylactic purposes, in particular genetic immunization. Among the particularly preferred embodiments of the invention are naturally occurring allelic variants the polynucleotides set forth in the Sequence Listing and polypeptides encoded thereby.

In accordance with yet another aspect of the invention, there are provided inhibitors to such polypeptides, useful as antibacterial agents, including, for example, antibodies.

In accordance with certain preferred embodiments of the invention, there are provided products, compositions and methods for assessing expression of the sequences the Sequence Listing, treating disease, for example, otitis media, conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleural empyema and endocarditis, and most particularly meningitis, such as for example infection of cerebrospinal fluid, assaying genetic variation, and

administering a polypeptide or polynucleotide of the invention to an organism to raise an immunological response against a bacteria, especially a *Streptococcus pneumoniae* bacteria.

In accordance with certain preferred embodiments of this and other aspects of the invention there are provided polynucleotides that hybridize to polynucleotide sequences of the invention, particularly under stringent conditions.

In certain preferred embodiments of the invention there are provided antibodies against polypeptides of the invention.

In other embodiments of the invention there are provided methods for identifying compounds which bind to or otherwise interact with and inhibit or activate an activity of a polypeptide or polynucleotide of the invention comprising: contacting a polypeptide or polynucleotide of the invention with a compound to be screened under conditions to permit binding to or other interaction between the compound and the polypeptide or polynucleotide to assess the binding to or other interaction with the compound, such binding or interaction being associated with a second component capable of providing a detectable signal in response to the binding or interaction of the polypeptide or polynucleotide with the compound; and determining whether the compound binds to or otherwise interacts with and activates or inhibits an activity of the polypeptide or polynucleotide by detecting the presence or absence of a signal generated from the binding or interaction of the compound with the polypeptide or polynucleotide.

In accordance with yet another aspect of the invention, there are provided agonists and antagonists of the polynucleotide and/or polypeptides of the invention, preferably bacteriostatic or bacteriocidal agonists and antagonists.

In a further aspect of the invention there are provided compositions comprising a polynucleotide or a polypeptide of the invention for administration to a cell or to a multicellular organism.

Various changes and modifications within the spirit and scope of the disclosed invention will become readily apparent to those skilled in the art from reading the following descriptions and from reading the other parts of the present disclosure.

Detailed Description of the Invention:

Each of the DNA sequences provided herein may be used in the discovery and development of antibacterial compounds. Because each of the sequences contains an open reading frame (ORF) with appropriate initiation and termination codons, the encoded protein upon expression can be used as a target for the screening of antimicrobial drugs. Additionally, the DNA sequences encoding preferably the amino terminal regions of the encoded protein or the Shine-Delgarno region can be used to construct antisense sequences

to control the expression of the coding sequence of interest. Furthermore, many of the sequences disclosed herein also provide regions upstream and downstream from the encoding sequence. These sequences are useful as a source of regulatory elements for the control of bacterial gene expression. Such sequences are conveniently isolated by 5 restriction enzyme action or synthesized chemically and introduced, for example, into promoter identification strains. These strains contain a reporter structural gene sequence located downstream from a restriction site such that if an active promoter is inserted, the reporter gene will be expressed.

Although each of the sequences may be employed as described above, this 10 invention also provides several means for identifying particularly useful target genes. The first of these approaches entails searching appropriate databases for sequence matches in related organisms. Thus, if a homologue exists, the Streptococcal-like form of this gene would likely play an analogous role. For example, a Streptococcal protein identified as homologous to a cell surface protein in another organism would be useful as a vaccine 15 candidate. To the extent such homologies have been identified for the sequences disclosed herein they are reported along with the encoding sequence.

Recently techniques have become available to evaluate temporal gene expression in bacteria, particularly as it applies to viability under laboratory and infection conditions. A number of methods can be used to identify genes which are essential to survival *per se*, or 20 essential to the establishment/maintenance of an infection. Identification of an ORF unknown by one of these methods yields additional information about its function and permits the selection of such an ORF for further development as a screening target. Briefly, these approaches include:

1) Signature Tagged Mutagenesis (STM)

25 This technique is described by Hensel *et al.*, *Science* 269: 400-403(1995), the contents of which is incorporated by reference for background purposes. Signature tagged mutagenesis identifies genes necessary for the establishment/maintenance of infection in a given infection model.

30 The basis of the technique is the random mutagenesis of target organism by various means (e.g., transposons) such that unique DNA sequence tags are inserted in close proximity to the site of mutation. The tags from a mixed population of bacterial mutants and bacteria recovered from an infected hosts are detected by amplification, radiolabeling and hybridisation analysis. Mutants attenuated in virulence are revealed by absence of the tag from the pool of bacteria recovered from infected hosts.

In Streptococcus pneumoniae, because the transposon system is less well developed, a more efficient way of creating the tagged mutants is to use the insertion-duplication mutagenesis technique as described by Morrison et al., J. Bacteriol. 159:870 (1984) the contents of which is incorporated by reference for background purposes.

5 **2) In Vivo Expression Technology (IVET)**

This technique is described by Camilli et al., Proc. Nat'l. Acad. Sci. USA. 91:2634-2638 (1994), the contents of which is incorporated by reference for background purposes. IVET identifies genes up-regulated during infection when compared to laboratory cultivation, implying an important role in infection. ORF identified by this technique are implied to have a significant role in infection establishment/maintenance.

In this technique random chromosomal fragments of target organism are cloned upstream of a promoter-less recombinase gene in a plasmid vector. This construct is introduced into the target organism which carries an antibiotic resistance gene flanked by resolvase sites. Growth in the presence of the antibiotic removes from the population those fragments cloned into the plasmid vector capable of supporting transcription of the recombinase gene and therefore have caused loss of antibiotic resistance. The resistant pool is introduced into a host and at various times after infection bacteria may be recovered and assessed for the presence of antibiotic resistance. The chromosomal fragment carried by each antibiotic sensitive bacterium should carry a promoter or portion of a gene normally upregulated during infection. Sequencing upstream of the recombinase gene allows identification of the up regulated gene.

20 **3) Differential display**

This technique is described by Chuang et al., J. Bacteriol. 175:2026-2036 (1993), the contents of which is incorporated by reference for background purposes. This method identifies those genes which are expressed in an organism by identifying mRNA present using randomly-primed RT-PCR. By comparing pre-infection and post infection profiles, genes up and down regulated during infection can be identified and the RT-PCR product sequenced and matched to ORF 'unknowns'.

4) Generation of conditional lethal mutants by transposon mutagenesis.

- This technique, described by de Lorenzo, V. et al., Gene 123:17-24 (1993); Neuwald, A. F. et al., Gene 125: 69-73(1993); and Takiff, H. E. et al., J. Bacteriol. 174:1544-1553(1992), the contents of which is incorporated by reference for background purposes, identifies genes whose expression are essential for cell viability.
- In this technique transposons carrying controllable promoters, which provide transcription outward from the transposon in one or both directions, are generated. Random insertion of these transposons into target organisms and subsequent isolation of insertion mutants in the presence of inducer of promoter activity ensures that insertions which separate promoter from coding region of a gene whose expression is essential for cell viability will be recovered. Subsequent replica plating in the absence of inducer identifies such insertions, since they fail to survive. Sequencing of the flanking regions of the transposon allows identification of site of insertion and identification of the gene disrupted. Close monitoring of the changes in cellular processes/morphology during growth in the absence of inducer yields information on likely function of the gene. Such monitoring could include flow cytometry (cell division, lysis, redox potential, DNA replication), incorporation of radiochemically labeled precursors into DNA, RNA, protein, lipid, peptidoglycan, monitoring reporter enzyme gene fusions which respond to known cellular stresses.
- 5) Generation of conditional lethal mutants by chemical mutagenesis.

This technique is described by Beckwith, J. Methods in Enzymology 204: 3-18(1991), the contents of which are incorporated herein by reference for background purposes. In this technique random chemical mutagenesis of target organism, growth at temperature other than physiological temperature (permissive temperature) and subsequent replica plating and growth at different temperature (e.g. 42°C to identify ts, 25°C to identify cs) are used to identify those isolates which now fail to grow (conditional mutants). As above close monitoring of the changes upon growth at the non-permissive temperature yields information on the function of the mutated gene. Complementation of conditional lethal mutation by library from target organism and sequencing of complementing gene allows matching with unknown ORF.

6) RT-PCR

Streptococcus pneumoniae messenger RNA is isolated from bacterial infected tissue e.g. 48 hour murine lung infections, and the amount of each mRNA species assessed by reverse transcription of the RNA sample primed with random hexanucleotides followed by PCR

with gene specific primer pairs. The determination of the presence and amount of a particular mRNA species by quantification of the resultant PCR product provides information on the bacterial genes which are transcribed in the infected tissue. Analysis of gene transcription can be carried out at different times of infection to gain a detailed knowledge of gene regulation in bacterial pathogenesis allowing for a clearer understanding of which gene products represent targets for screens for novel antibacterials. Because of the gene specific nature of the PCR primers employed it should be understood that the bacterial mRNA preparation need not be free of mammalian RNA. This allows the investigator to carry out a simple and quick RNA preparation from infected tissue to obtain bacterial mRNA species which are very short lived in the bacterium (in the order of 2 minute halflives). Optimally the bacterial mRNA is prepared from infected murine lung tissue by mechanical disruption in the presence of TRIzole (GIBCO-BRL) for very short periods of time, subsequent processing according to the manufacturers of TRIzole reagent and DNAase treatment to remove contaminating DNA. Preferably the process is optimised by finding those conditions which give a maximum amount of *S.pneumoniae* 16S ribosomal RNA as detected by probing Northerns with a suitably labelled sequence specific oligonucleotide probe. Typically a 5' dye labelled primer is used in each PCR primer pair in a PCR reaction which is terminated optimally between 8 and 25 cycles. The PCR products are separated on 6% polyacrylamide gels with detection and quantification using GeneScanner (manufactured by ABI).

Each of these techniques may have advantages or disadvantage depending on the particular application. The skilled artisan would choose the approach that is the most relevant with the particular end use in mind. For example, some genes might be recognised as essential for infection but in reality are only necessary for the initiation of infection and so their products would represent relatively unattractive targets for antibacterials developed to cure established and chronic infections.

Use of the of these technologies when applied to the ORFs of the present invention enables identification of bacterial proteins expressed during infection, inhibitors of which would have utility in anti-bacterial therapy.

30 *Streptococcus pneumoniae*, strain 0100993 has been deposited at the National Collection of Industrial and Marine Bacteria Ltd. (NCIMB), Aberdeen, Scotland under NCIMB number 40794 on 11 April 1996, and a *Streptococcus pneumoniae*, strain 0100993 DNA library in *E. coli* was similarly deposited on 17 April 1996 under NCIMB number 40800.

The nucleotide sequences disclosed herein can be obtained by synthetic chemical techniques known in the art or can be obtained from *Streptococcus pneumoniae*, strain 0100993 by probing a DNA preparation with probes constructed from the particular sequences disclosed herein. Alternatively, oligonucleotides derived from a disclosed sequence can act as PCR primers in a process of PCR-based cloning of the sequence from a bacterial genomic source. It is recognised that such sequences will also have utility in diagnosis of the stage of infection and type of infection the pathogen has attained.

To obtain the polynucleotide encoding the protein using the DNA sequence given herein typically a library of clones of chromosomal DNA of *Streptococcus pneumoniae*, strain 0100993 in *E. coli* or some other suitable host is probed with a radiolabelled oligonucleotide, preferably a 17mer or longer, derived from the partial sequence. Clones carrying DNA identical to that of the probe can then be distinguished using high stringency washes. By sequencing the individual clones thus identified with sequencing primers designed from the original sequence it is then possible to extend the sequence in both directions to determine the full gene sequence. Conveniently such sequencing is performed using denatured double stranded DNA prepared from a plasmid clone. Suitable techniques are described by Maniatis, T., Fritsch, E.F. and Sambrook, J. in MOLECULAR CLONING, A Laboratory Manual, 2nd edition, 1989, Cold Spring Harbor Laboratory (see: Screening By Hybridization 1.90 and Sequencing Denatured Double-Stranded DNA Templates 20 13.70).

A polynucleotide of the present invention may be in the form of RNA or in the form of DNA, which DNA includes cDNA, genomic DNA, and synthetic DNA. The DNA may be double-stranded or single-stranded, and if single stranded may be the coding strand or non-coding (anti-sense) strand. The coding sequence which encodes the polypeptide 25 may be identical to the coding sequence shown or may be a different coding sequence which coding sequence, as a result of the redundancy or degeneracy of the genetic code, encoding the same polypeptide.

The present invention includes variants of the hereinabove described polynucleotides which encode fragments, analogues and derivatives of the polypeptide 30 characterized by the deduced amino acid sequence given herein. The variant of the polynucleotide may be a naturally occurring allelic variant of the polynucleotide or a non-naturally occurring variant of the polynucleotide. In addition to the standard A, G, C, T/U representations for nucleic acid bases, the term "N" is also used. "N" means that any of the four DNA or RNA bases may appear at such a designated position in the DNA or RNA

sequence, except that N cannot be a base that when taken in combination with adjacent nucleotide positions, when read in the correct reading frame, would have the effect of generating a premature termination codon in such reading frame.

Thus, the present invention includes polynucleotides encoding the same 5 polypeptide characterized by the deduced amino acid sequence given herein as well as variants of such polynucleotides which variants encode for a fragment, derivative or analogue of the polypeptide. Such nucleotide variants include deletion variants, substitution variants and addition or insertion variants.

The polynucleotide may have a coding sequence which is a naturally occurring 10 allelic variant of the coding sequence characterized by the DNA sequence disclosed herein. As known in the art, an allelic variant is an alternate form of a polynucleotide sequence which may have a substitution, deletion or addition of one or more nucleotides, which does not substantially alter the function of the encoded polypeptide.

The polynucleotide which encodes for the mature polypeptide, may include only 15 the coding sequence for the mature polypeptide or the coding sequence for the mature polypeptide and additional coding sequence such as a leader or secretory sequence or a proprotein sequence.

Thus, the term "polynucleotide encoding a polypeptide" encompasses a 20 polynucleotide which includes only coding sequence for the polypeptide as well as a polynucleotide which includes additional coding and/or non-coding sequence.

The present invention therefore includes polynucleotides, wherein the coding sequence for the mature polypeptide may be fused in the same reading frame to a 25 polynucleotide sequence which aids in expression and secretion of a polypeptide from a host cell, for example, a leader sequence which functions as a secretory sequence for controlling transport of a polypeptide from the cell. The polypeptide having a leader sequence is a proprotein and may have the leader sequence cleaved by the host cell to form the mature form of the polypeptide. The polynucleotides may also encode for a proprotein which is the mature protein plus additional 5' amino acid residues. A mature protein having a prosequence is a proprotein and may be an inactive form of the protein. Once the 30 prosequence is cleaved an active mature protein remains.

Thus, for example, the polynucleotide of the present invention may code for a mature protein, or for a protein having a prosequence or for a protein having both a prosequence and a presequence (leader sequence). Further, the amino acid sequences provided herein show a methionine residue at the NH₂-terminus. It is appreciated, however,

that during post-translational modification of the peptide, this residue may be deleted. Accordingly, this invention contemplates the use of both the methionine-containing and the methionineless amino terminal variants of each protein disclosed herein.

- The polynucleotides of the present invention may also have the coding sequence fused in frame to a marker sequence at either the 5' or 3' terminus of the gene which allows for purification of the polypeptide of the present invention. The marker sequence may be a hexa-histidine tag supplied by the pQE series of vectors (supplied commercially by Qiagen Inc.) to provide for purification of the polypeptide fused to the marker in the case of a bacterial host.
- 10 The present invention further relates to polynucleotides which hybridize to the hereinabove-described sequences if there is at least 50% and preferably at least 70% identity between the sequences. The present invention particularly relates to polynucleotides, particularly Streptococcal polynucleotides, which hybridize under stringent conditions to the hereinabove-described polynucleotides . As herein used, the term "stringent conditions" means hybridization will occur only if there is at least 95% and preferably at least 97% identity between the sequences. The polynucleotides which hybridize to the hereinabove described polynucleotides in a preferred embodiment encode polypeptides which retain substantially the same biological function or activity as the polypeptide characterised by the deduced amino acid sequence given herein. An example of stringent hybridization
- 20 conditions is overnight incubation at 42°C in a solution comprising: 50% formamide, 5x SSC (150mM NaCl, 15mM trisodium citrate), 50 mM sodium phosphate (pH7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 micrograms/ml denatured, sheared salmon sperm DNA, followed by washing the hybridization support in 0.1x SSC at about 65°C. Hybridization and wash conditions are well known and exemplified in Sambrook, *et al.*,
- 25 Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, N.Y., (1989), particularly Chapter 11 therein.

The invention also provides a polynucleotide consisting essentially of a polynucleotide sequence obtainable by screening an appropriate library containing the complete gene for a polynucleotide sequence selected from the group consisting of the 30 polynucleotides of the Sequence Listing under stringent hybridization conditions with a probe having the sequence of said polynucleotide sequence set forth in said polynucleotide of the Sequence Listing or a fragment thereof; and isolating said DNA sequence. Fragments useful for obtaining such a polynucleotide include, for example, probes and primers described elsewhere herein.

"Identity," as known in the art and used herein, is a relationship between two or more polypeptide sequences or two or more polynucleotide sequences, as determined by comparing the sequences. In the art, "identity" also means the degree of sequence relatedness between polypeptide or polynucleotide sequences, as the case may be, as determined by the match between strings of such sequences. "Identity" and "similarity" can be readily calculated by known methods, including but not limited to those described in (*Computational Molecular Biology*, Lesk, A.M., ed., Oxford University Press, New York, 1988; *Biocomputing: Informatics and Genome Projects*, Smith, D.W., ed., Academic Press, New York, 1993; *Computer Analysis of Sequence Data*, Part I, Griffin, A.M., and Griffin, H.G., eds., 5 Humana Press, New Jersey, 1994; *Sequence Analysis in Molecular Biology*, von Heinje, G., Academic Press, 1987; and *Sequence Analysis Primer*, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991; and Carillo, H., and Lipman, D., *SIAM J. Applied Math.*, 48: 1073 (1988). Preferred methods to determine identity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity 10 are codified in publicly available computer programs. Preferred computer program methods to determine identity and similarity between two sequences include, but are not limited to, the GCG program package (Devereux, J., et al., *Nucleic Acids Research* 12(1): 387 (1984)), BLASTP, BLASTN, and FASTA (Altschul, S.F. et al., *J. Molec. Biol.* 215: 403-410 (1990)). The BLAST X program is publicly available from NCBI and other sources (*BLAST* 15 20 *Manual*, Altschul, S., et al., NCBI NLM NIH Bethesda, MD 20894; Altschul, S., et al., *J. Mol. Biol.* 215: 403-410 (1990)).

As an illustration, by a polynucleotide having a nucleotide sequence having at least, for example, 95% "identity" to a reference nucleotide sequence selected from the group consisting of the polynucleotide of the Sequence Listing is intended that the nucleotide 25 sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another 30 nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. These mutations of the reference sequence may occur at the 5' or 3' terminal positions of the reference nucleotide sequence or anywhere between those terminal positions, interspersed either individually among

nucleotides in the reference sequence or in one or more contiguous groups within the reference sequence.

Similarly, by a polypeptide having an amino acid sequence having at least, for example, 95% identity to a reference amino acid sequence of selected from the 5 group consisting of the amino acids of the Sequence Listing is intended that the amino acid sequence of the polypeptide is identical to the reference sequence except that the polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the reference amino acid. In other words, to obtain a 10 polypeptide having an amino acid sequence at least 95% identical to a reference amino acid sequence, up to 5% of the amino acid residues in the reference sequence may be deleted or substituted with another amino acid, or a number of amino acids up to 5% of the total amino acid residues in the reference sequence may be inserted 15 into the reference sequence. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

The deposit referred to herein will be maintained under the terms of the Budapest Treaty on the International Recognition of the Deposit of Micro-organisms for purposes of 20 Patent Procedure. These deposits are provided merely as convenience to those of skill in the art and are not an admission that a deposit is required under 35 U.S.C. §112. The sequence of the polynucleotides contained in the deposited material, as well as the amino acid sequence of the polypeptides encoded thereby, are incorporated herein by reference and are controlling in the event of any conflict with any description of sequences herein. A 25 license may be required to make, use or sell the deposited material, and no such license is hereby granted.

The terms "fragment," "derivative" and "analogue" when referring to the 30 polypeptide characterized by the deduced amino acid sequence herein, means a polypeptide which retains essentially the same biological function or activity as such polypeptide. Thus, an analogue includes a proprotein which can be activated by cleavage of the proprotein portion to produce an active mature polypeptide.

The polypeptide of the present invention may be a recombinant polypeptide, a natural polypeptide or a synthetic polypeptide, preferably a recombinant polypeptide.

The fragment, derivative or analogue of the polypeptide characterized by the deduced amino acid sequence herein may be (i) one in which one or more of the amino acid residues are substituted with a conserved or non-conserved amino acid residue (preferably a conserved amino acid residue) and such substituted amino acid residue may or may not be 5 one encoded by the genetic code, or (ii) one in which one or more of the amino acid residues includes a substituent group, or (iii) one in which the polypeptide is fused with another compound, such as a compound to increase the half-life of the polypeptide (for example, polyethylene glycol), or (iv) one in which the additional amino acids are fused to 10 the polypeptide, such as a leader or secretory sequence or a sequence which is employed for purification of the polypeptide or a proprotein sequence. Such fragments, derivatives and analogues are deemed to be within the scope of those skilled in the art from the teachings herein.

The polypeptides and polynucleotides of the present invention are preferably provided in an isolated form, and preferably are purified to homogeneity. 15 The term "isolated" means that the material is removed from its original environment (e.g., the natural environment if it is naturally occurring). For example, a naturally-occurring polynucleotide or polypeptide present in a living animal is not isolated, but the same polynucleotide or polypeptide, separated from some or all of the coexisting materials in the natural system, is isolated. Such polynucleotides could be part of a vector 20 and/or such polynucleotides or polypeptides could be part of a composition, and still be isolated in that such vector or composition is not part of its natural environment.

The present invention also relates to vectors which include polynucleotides of the present invention, host cells which are genetically engineered with vectors of the invention and the production of polypeptides of the invention by recombinant techniques.

25 In accordance with yet a further aspect of the present invention, there is therefore provided a process for producing the polypeptide of the invention by recombinant techniques by expressing a polynucleotide encoding said polypeptide in a host and recovering the expressed product. Alternatively, the polypeptides of the invention can be synthetically produced by conventional peptide synthesizers.

30 Host cells are genetically engineered (transduced or transformed or transfected) with the vectors of this invention which may be, for example, a cloning vector or an expression vector. The vector may be, for example, in the form of a plasmid, a cosmid, a phage, etc. The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying the

genes. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

- Suitable expression vectors include chromosomal, nonchromosomal and synthetic
5 DNA sequences, e.g., bacterial plasmids; phage DNA; baculovirus; yeast plasmids; vectors derived from combinations of plasmids and phage DNA. However, any other vector may be used as long as it is replicable and viable in the host.

- The appropriate DNA sequence may be inserted into the vector by a variety of procedures. In general, the DNA sequence is inserted into an appropriate restriction
10 endonuclease site(s) by procedures known in the art.

- The DNA sequence in the expression vector is operatively linked to an appropriate expression control sequence(s) (promoter) to direct mRNA synthesis. As representative examples of such promoters, there may be mentioned: LTR or SV40 promoter, the *E. coli*. *lac* or *trp*, the phage lambda P_L promoter and other promoters known to control expression
15 of genes in eukaryotic or prokaryotic cells or their viruses. The expression vector also contains a ribosome binding site for translation initiation and a transcription terminator. The vector may also include appropriate sequences for amplifying expression.

- In addition, the expression vectors preferably contain one or more selectable marker genes to provide a phenotypic trait for selection of transformed host cells such as
20 dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, or such as tetracycline or ampicillin resistance in *E. coli*.

- The gene can be placed under the control of a promoter, ribosome binding site (for bacterial expression) and, optionally, an operator (collectively referred to herein as "control" elements), so that the DNA sequence encoding the desired protein is transcribed into RNA
25 in the host cell transformed by a vector containing this expression construction. The coding sequence may or may not contain a signal peptide or leader sequence. The polypeptides of the present invention can be expressed using, for example, the *E. coli* tac promoter or the protein A gene (spa) promoter and signal sequence. Leader sequences can be removed by the bacterial host in post-translational processing. See, e.g., U.S. Patent Nos. 4,431,739;
30 4,425,437; 4,338,397. Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are PKK232-8 and PCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda P_R, P_L and trp. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and

mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art.

- In addition to control sequences, it may be desirable to add regulatory sequences which allow for regulation of the expression of the protein sequences relative to the growth
- 5 of the host cell. Regulatory sequences are known to those of skill in the art, and examples include those which cause the expression of a gene to be turned on or off in response to a chemical or physical stimulus, including the presence of a regulatory compound. Other types of regulatory elements may also be present in the vector, for example, enhancer sequences.
- 10 An expression vector is constructed so that the particular coding sequence is located in the vector with the appropriate regulatory sequences, the positioning and orientation of the coding sequence with respect to the control sequences being such that the coding sequence is transcribed under the "control" of the control sequences (i.e., RNA polymerase which binds to the DNA molecule at the control sequences transcribes the coding sequence). Modification of the coding sequences may be desirable to achieve this end. For example, in some cases it may be necessary to modify the sequence so that it may be attached to the control sequences with the appropriate orientation; i.e., to maintain the reading frame. The control sequences and other regulatory sequences may be ligated to the coding sequence prior to insertion into a vector, such as the cloning vectors described
- 15 above. Alternatively, the coding sequence can be cloned directly into an expression vector which already contains the control sequences and an appropriate restriction site.
- 20

Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an N-terminal

25 identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product.

The vector containing the appropriate DNA sequence as hereinabove described, as well as an appropriate promoter or control sequence, may be employed to transform an appropriate host to permit the host to express the protein.

More particularly, the present invention also includes recombinant constructs comprising one or more of the sequences as broadly described above. The constructs comprise a vector, such as a plasmid or viral vector, into which a sequence of the invention has been inserted, in a forward or reverse orientation. In a preferred aspect of this embodiment, the construct further comprises regulatory sequences, including, for example, a promoter, operably linked to the sequence. Large numbers of suitable vectors and promoters are known to those of skill in the art, and are commercially available. The following vectors are provided by way of example. Bacterial: pET-3 vectors (Stratagene), pQE70, pQE60, pQE-9 (Qiagen), pbs, pD10, phagescript, psiX174, pbluescript SK, pbsks, pNH8A, pNH16a, pNH18A, pNH46A (Stratagene); ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pBlueBacIII (Invitrogen), pWLNEO, pSV2CAT, pOG44, pXT1, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia). However, any other plasmid or vector may be used as long as they are replicable and viable in the host.

Examples of recombinant DNA vectors for cloning and host cells which they can transform include the bacteriophage *I* (*E. coli*), pBR322 (*E. coli*), pACYC177 (*E. coli*), pKT230 (gram-negative bacteria), pGV1106 (gram-negative bacteria), pLAFR1 (gram-negative bacteria), pME290 (non-*E. coli* gram-negative bacteria), pHV14 (*E. coli* and *Bacillus subtilis*), pBD9 (*Bacillus*), pIJ61 (*Streptomyces*), pUC6 (*Streptomyces*), YIp5 (*Saccharomyces*), a baculovirus insect cell system, YCp19 (*Saccharomyces*). See, generally, "DNA Cloning": Vols. I & II, Glover *et al.* ed. IRL Press Oxford (1985) (1987) and; T. Maniatis *et al.* ("Molecular Cloning" Cold Spring Harbor Laboratory (1982).

In some cases, it may be desirable to add sequences which cause the secretion of the polypeptide from the host organism, with subsequent cleavage of the secretory signal.

Polypeptides can be expressed in host cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, *et al.*, Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, N.Y., (1989), the disclosure of which is hereby incorporated by reference.

Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period.

Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use 5 of cell lysing agents, such methods are well known to those skilled in the art.

Depending on the expression system and host selected, the polypeptide of the present invention may be produced by growing host cells transformed by an expression vector described above under conditions whereby the polypeptide of interest is expressed. The polypeptide is then isolated from the host cells and purified. If the expression system 10 secretes the polypeptide into growth media, the polypeptide can be purified directly from the media. If the polypeptide is not secreted, it is isolated from cell lysates or recovered from the cell membrane fraction. Where the polypeptide is localized to the cell surface, whole cells or isolated membranes can be used as an assayable source of the desired gene product. Polypeptide expressed in bacterial hosts such as *E. coli* may require isolation from 15 inclusion bodies and refolding. Where the mature protein has a very hydrophobic region which leads to an insoluble product of overexpression, it may be desirable to express a truncated protein in which the hydrophobic region has been deleted. The selection of the appropriate growth conditions and recovery methods are within the skill of the art.

The polypeptide can be recovered and purified from recombinant cell cultures by 20 methods including ammonium sulphate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography 25 (HPLC) can be employed for final purification steps.

Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated. Polypeptides of the invention may also include an initial methionine amino acid residue.

A "replicon" is any genetic element (e.g., plasmid, chromosome, virus) that 30 functions as an autonomous unit of DNA replication *in vivo*; i.e., capable of replication under its own control.

A "vector" is a replicon, such as a plasmid, phage, or cosmid, to which another DNA segment may be attached so as to bring about the replication of the attached segment.

A "double-stranded DNA molecule" refers to the polymeric form of deoxyribonucleotides (bases adenine, guanine, thymine, or cytosine) in a double-stranded helix, both relaxed and supercoiled. This term refers only to the primary and secondary structure of the molecule, and does not limit it to any particular tertiary forms. Thus, this 5 term includes double-stranded DNA found, *inter alia*, in linear DNA molecules (e.g., restriction fragments), viruses, plasmids, and chromosomes. In discussing the structure of particular double-stranded DNA molecules, sequences may be described herein according to the normal convention of giving only the sequence in the 5' to 3' direction along the nontranscribed strand of DNA (i.e., the strand having the sequence homologous to the 10 mRNA).

A DNA "coding sequence of" or a "nucleotide sequence encoding" a particular protein, is a DNA sequence which is transcribed and translated into a polypeptide when placed under the control of appropriate regulatory sequences.

A "promoter sequence" is a DNA regulatory region capable of binding RNA 15 polymerase in a cell and initiating transcription of a downstream (3' direction) coding sequence. For purposes of defining the present invention, the promoter sequence is bound at the 3' terminus by a translation start codon (e.g., ATG) of a coding sequence and extends upstream (5' direction) to include the minimum number of bases or elements necessary to initiate transcription at levels detectable above background. Within the promoter sequence 20 will be found a transcription initiation site (conveniently defined by mapping with nuclease S1), as well as protein binding domains (consensus sequences) responsible for the binding of RNA polymerase. Eukaryotic promoters will often, but not always, contain "TATA" boxes and "CAT" boxes. Prokaryotic promoters contain Shine-Dalgarno sequences in addition to the -10 and -35 consensus sequences.

DNA "control sequences" refers collectively to promoter sequences, ribosome 25 binding sites, polyadenylation signals, transcription termination sequences, upstream regulatory domains, enhancers, and the like, which collectively provide for the expression (i.e., the transcription and translation) of a coding sequence in a host cell.

A control sequence "directs the expression" of a coding sequence in a cell when 30 RNA polymerase will bind the promoter sequence and transcribe the coding sequence into mRNA, which is then translated into the polypeptide encoded by the coding sequence.

A "host cell" is a cell which has been transformed or transfected, or is capable of transformation or transfection by an exogenous DNA sequence.

A cell has been "transformed" by exogenous DNA when such exogenous DNA has been introduced inside the cell membrane. Exogenous DNA may or may not be integrated (covalently linked) into chromosomal DNA making up the genome of the cell. In prokaryotes and yeasts, for example, the exogenous DNA may be maintained on an episomal element, such as a plasmid. With respect to eukaryotic cells, a stably transformed or transfected cell is one in which the exogenous DNA has become integrated into the chromosome so that it is inherited by daughter cells through chromosome replication. This stability is demonstrated by the ability of the eukaryotic cell to establish cell lines or clones comprised of a population of daughter cell containing the exogenous DNA.

10 A "clone" is a population of cells derived from a single cell or common ancestor by mitosis. A "cell line" is a clone of a primary cell that is capable of stable growth *in vitro* for many generations.

15 A "heterologous" region of a DNA construct is an identifiable segment of DNA within or attached to another DNA molecule that is not found in association with the other molecule in nature.

This invention is also related to the use of the polynucleotides of the invention for use as diagnostic reagents. Detection of a polynucleotide or polypeptide of the invention in a eukaryote, particularly a mammal, and especially a human, will provide a diagnostic method for diagnosis of a disease. Eukaryotes (herein also "individual(s)"), particularly mammals, and especially humans, infected with an organism comprising a polynucleotide of the invention may be detected at the nucleic acid level by a variety of techniques.

Nucleic acids for diagnosis may be obtained from an infected individual's cells and tissues, such as bone, blood, muscle, cartilage, and skin. Genomic DNA may be used directly for detection or may be amplified enzymatically by using PCR or other amplification technique prior to analysis. RNA or cDNA may also be used in the same ways. Using amplification, characterization of the species and strain of prokaryote present in an individual, may be made by an analysis of the genotype of the prokaryote gene. Deletions and insertions can be detected by a change in size of the amplified product in comparison to the genotype of a reference sequence. Point mutations can be identified by hybridizing amplified DNA to labeled polynucleotide sequences of the invention. Perfectly matched sequences can be distinguished from mismatched duplexes by RNase digestion or by differences in melting temperatures. DNA sequence differences may also be detected by alterations in the electrophoretic mobility of the DNA fragments in gels, with or without denaturing agents, or by direct DNA sequencing. See, e.g., Myers et al., *Science*, 230: 1242 (1985). Sequence changes at specific locations also may be

revealed by nuclease protection assays, such as RNase and S1 protection or a chemical cleavage method. See, e.g., Cotton et al., *Proc. Natl. Acad. Sci., USA*, 85: 4397-4401 (1985).

Cells carrying mutations or polymorphisms in the gene of the invention may also be detected at the DNA level by a variety of techniques, to allow for serotyping, for example. For example, RT-PCR can be used to detect mutations. It is particularly preferred to used RT-PCR in conjunction with automated detection systems, such as, for example, GeneScan. RNA or cDNA may also be used for the same purpose, PCR or RT-PCR. As an example, PCR primers complementary to a nucleic acid encoding a polypeptide of the invention can be used to identify and analyze mutations. These primers may be used for, among other things, amplifying DNA isolated from a sample derived from an individual. The primers may be used to amplify the gene isolated from an infected individual such that the gene may then be subject to various techniques for elucidation of the DNA sequence. In this way, mutations in the DNA sequence may be detected and used to diagnose infection and to serotype and/or classify the infectious agent.

The invention further provides a process for diagnosing, disease, preferably bacterial infections, more preferably infections by *Streptococcus pneumoniae*, comprising determining from a sample derived from an individual a increased level of expression of polynucleotide having a sequence set forth in the Sequence Listing or a sequence of the invention. Increased or decreased expression of a polynucleotide of the invention can be measured using any one of the methods well known in the art for the quantitation of polynucleotides, such as, for example, amplification, PCR, RT-PCR, RNase protection, Northern blotting and other hybridization methods.

In addition, a diagnostic assay in accordance with the invention for detecting over-expression of a polypeptide of the invention compared to normal control tissue samples may be used to detect the presence of an infection, for example. Assay techniques that can be used to determine levels of a polypeptide of the invention, in a sample derived from a host are well-known to those of skill in the art. Such assay methods include radioimmunoassays, competitive-binding assays, Western Blot analysis and ELISA assays.

In accordance with yet a further aspect of the present invention, there is provided the use of a polypeptide of the invention for therapeutic or prophylactic purposes, for example, as an antibacterial agent or a vaccine.

In accordance with another aspect of the present invention, there is provided the use of a polynucleotide of the invention for therapeutic or prophylactic purposes, in particular genetic immunisation.

In accordance with yet another aspect of the present invention, there are provided inhibitors to such polypeptides, useful as antibacterial agents. In particular, there are provided antibodies against such polypeptides.

Polypeptides of the invention may also be used to assess the binding of small molecule substrates and ligands in, for example, cells, cell-free preparations, chemical libraries, and natural product mixtures. These substrates and ligands may be natural substrates and ligands or may be structural or functional mimetics. See, e.g., Coligan *et al.*, *Current Protocols in Immunology* 1(2): Chapter 5 (1991).

The invention also provides a method of screening compounds to identify those which enhance (agonist) or block (antagonist) the action of polypeptides or polynucleotides of the invention, particularly those compounds that are bacteriostatic and/or bacteriocidal. The method of screening may involve high-throughput techniques. For example, to screen for agonists or antagonists, a synthetic reaction mix, a cellular compartment, such as a membrane, cell envelope or cell wall, or a preparation of any thereof, comprising a polypeptide of the invention and a labeled substrate or ligand of such polypeptide is incubated in the absence or the presence of a candidate molecule that may be an agonist or antagonist of a polypeptide of the invention. The ability of the candidate molecule to agonize or antagonize a polypeptide of the invention is reflected in decreased binding of the labeled ligand or decreased production of product from such substrate. Molecules that bind gratuitously, i.e., without inducing the effects of a polypeptide of the invention are most likely to be good antagonists. Molecules that bind well and increase the rate of product production from substrate are agonists. Detection of the rate or level of production of product from substrate may be enhanced by using a reporter system. Reporter systems that may be useful in this regard include but are not limited to colorimetric labeled substrate converted into product, a reporter gene that is responsive to changes in polynucleotide or polypeptide activity, and binding assays known in the art.

Another example of an assay for antagonists of a polypeptide of the invention is a competitive assay that combines such polypeptide and a potential antagonist with polypeptide-binding molecules, recombinant polypeptide-binding molecules, natural substrates or ligands, or substrate or ligand mimetics, under appropriate conditions for a competitive inhibition assay. Polypeptides of the invention can be labeled, such as by radioactivity or a colorimetric compound, such that the number of such polypeptide molecules bound to a binding molecule or converted to product can be determined accurately to assess the effectiveness of the potential antagonist.

Potential antagonists include small organic molecules, peptides, polypeptides and antibodies that bind to a polynucleotide or polypeptide of the invention and thereby inhibit or extinguish its activity. Potential antagonists also may be small organic molecules, a peptide, a polypeptide such as a closely related protein or antibody that binds the same sites on a binding molecule, without inducing an activities of a polypeptide of the invention, thereby preventing the action of such polypeptide by excluding it from binding.

5 Potential antagonists include a small molecule that binds to and occupies the binding site of the polypeptide thereby preventing binding to cellular binding molecules, such that normal biological activity is prevented. Examples of small molecules include but are not limited
10 to small organic molecules, peptides or peptide-like molecules. Other potential antagonists include antisense molecules (see Okano, *J. Neurochem.* 56: 560 (1991); *OLIGODEOXYNUCLEOTIDES AS ANTISENSE INHIBITORS OF GENE EXPRESSION*, CRC Press, Boca Raton, FL (1988), for a description of these molecules). Preferred potential antagonists include compounds related to and variants of the polypeptides of the invention.

15 Each of the DNA sequences provided herein may be used in the discovery and development of antibacterial compounds. The encoded protein, upon expression, can be used as a target for the screening of antibacterial drugs. Additionally, the DNA sequences encoding the amino terminal regions of the encoded protein or Shine-Delgarno or other translation facilitating sequences of the respective mRNA can be used to construct antisense
20 sequences to control the expression of the coding sequence of interest.

The invention also provides the use of the polypeptide, polynucleotide or inhibitor of the invention to interfere with the initial physical interaction between a pathogen and mammalian host responsible for sequelae of infection. In particular the molecules of the invention may be used: in the prevention of adhesion of bacteria, in particular gram positive
25 bacteria, to mammalian extracellular matrix proteins on in-dwelling devices or to extracellular matrix proteins in wounds; to block protein-mediated mammalian cell invasion by, for example, initiating phosphorylation of mammalian tyrosine kinases (Rosenshine *et al.*, *Infect. Immun.* 60:2211 (1992); to block bacterial adhesion between mammalian extracellular matrix proteins and bacterial proteins that mediate tissue damage and; to block
30 the normal progression of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or by other surgical techniques.

The antagonists and agonists of the invention may be employed, for instance, to inhibit and treat otitis media, conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleural

empyema and endocarditis, and most particularly meningitis, such as for example infection of cerebrospinal fluid.

Another aspect of the invention is a pharmaceutical composition comprising the above polypeptide, polynucleotide or inhibitor of the invention and a pharmaceutically acceptable carrier.

5 In a particular aspect the invention provides the use of an inhibitor of the invention as an antibacterial agent.

The invention further relates to the manufacture of a medicament for such uses.

10 The polypeptide may be used as an antigen for vaccination of a host to produce specific antibodies which have anti-bacterial action. This invention also contemplates the use of the DNA encoding the antigen as a component in a DNA vaccine as discussed more fully below.

15 The polypeptides or cells expressing them can be used as an immunogen to produce antibodies thereto. These antibodies can be, for example, polyclonal or monoclonal antibodies. The term antibodies also includes chimeric, single chain, and humanized antibodies, as well as Fab fragments, or the product of an Fab expression library. Various procedures known in the art may be used for the production of such antibodies and fragments.

20 Antibodies generated against the polypeptides of the present invention can be obtained by direct injection of the polypeptides into an animal or by administering the polypeptides to an animal, preferably a nonhuman. The antibody so obtained will then bind the polypeptides itself. In this manner, even a sequence encoding only a fragment of the polypeptides can be used to generate antibodies binding the whole native polypeptides. Such antibodies can then be used to isolate the polypeptide from tissue expressing that 25 polypeptide.

Polypeptide derivatives include antigenically or immunologically equivalent derivatives which form a particular aspect of this invention.

30 The term 'antigenically equivalent derivative' as used herein encompasses a polypeptide or its equivalent which will be specifically recognised by certain antibodies which, when raised to the protein or polypeptide according to the present invention, interfere with the interaction between pathogen and mammalian host.

The term 'immunologically equivalent derivative' as used herein encompasses a peptide or its equivalent which when used in a suitable formulation to raise antibodies in a

vertebrate, the antibodies act to interfere with the interaction between pathogen and mammalian host.

In particular derivatives which are slightly longer or slightly shorter than the native protein or polypeptide fragment of the present invention may be used. In addition,

- 5 polypeptides in which one or more of the amino acid residues are modified may be used. Such peptides may, for example, be prepared by substitution, addition, or rearrangement of amino acids or by chemical modification thereof. All such substitutions and modifications are generally well known to those skilled in the art of peptide chemistry.

- 10 The polypeptide, such as an antigenically or immunologically equivalent derivative or a fusion protein thereof is used as an antigen to immunize a mouse or other animal such as a rat or chicken. The fusion protein may provide stability to the polypeptide. The antigen may be associated, for example by conjugation, with an immunogenic carrier protein for example bovine serum albumin (BSA) or keyhole limpet haemocyanin (KLH). Alternatively a multiple antigenic peptide comprising multiple copies of the protein or 15 polypeptide, or an antigenically or immunologically equivalent polypeptide thereof may be sufficiently antigenic to improve immunogenicity so as to obviate the use of a carrier.

- 20 For preparation of monoclonal antibodies, any technique which provides antibodies produced by continuous cell line cultures can be used. Examples include the hybridoma technique (Kohler and Milstein, *Nature*, 256:495-497(1975)), the trioma technique, the human B-cell hybridoma technique (Kozbor et al., *Immunology Today* 4:72(1983)), and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole, et al., 1985, in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96).

- 25 Techniques described for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce single chain antibodies to immunogenic polypeptide products of this invention.

Using the procedure of Kohler and Milstein (*supra*, (1975)), antibody-containing cells from the immunised mammal are fused with myeloma cells to create hybridoma cells secreting monoclonal antibodies.

- 30 The hybridomas are screened to select a cell line with high binding affinity and favorable cross reaction with other Streptococcal species using one or more of the original polypeptide and/or the fusion protein. The selected cell line is cultured to obtain the desired Mab.

Hybridoma cell lines secreting the monoclonal antibody are another aspect of this invention.

Alternatively phage display technology could be utilised to select antibody genes with binding activities towards the polypeptide either from repertoires of PCR amplified v-genes of lymphocytes from humans screened for possessing anti-Fbp or from naive libraries (McCafferty, J. et al., *Nature* 348:552-554(1990), and Marks, J. et al., *Biotechnology* 5: 10:779-783(1992)). The affinity of these antibodies can also be improved by chain shuffling (Clackson, T. et al., *Nature* 352:624-628(1991)).

The antibody should be screened again for high affinity to the polypeptide and/or fusion protein.

As mentioned above, a fragment of the final antibody may be prepared.

10 The antibody may be either intact antibody of M_r approx 150,000 or a derivative of it, for example a Fab fragment or a Fv fragment as described in Skerra, A and Pluckthun, A., *Science* 240:1038-1040 (1988). If two antigen binding domains are present each domain may be directed against a different epitope - termed 'bispecific' antibodies.

15 The antibody of the invention may be prepared by conventional means for example by established monoclonal antibody technology (Kohler, G. and Milstein, C. (*supra*, (1975) or using recombinant means e.g. combinatorial libraries, for example as described in Huse, W.D. et al., *Science* 246:1275-1281 (1989).

20 Preferably the antibody is prepared by expression of a DNA polymer encoding said antibody in an appropriate expression system such as described above for the expression of polypeptides of the invention. The choice of vector for the expression system will be determined in part by the host, which may be a prokaryotic cell, such as *E. coli* (preferably strain B) or *Streptomyces sp.* or a eukaryotic cell, such as a mouse C127, mouse myeloma, human HeLa, Chinese hamster ovary, filamentous or unicellular fungi or insect cell. The host may also be a transgenic animal or a transgenic plant (for example, as described in 25 Hiatt, A. et al., *Nature* 340:76-78(1989). Suitable vectors include plasmids, bacteriophages, cosmids and recombinant viruses, derived from, for example, baculoviruses and vaccinia.

The Fab fragment may also be prepared from its parent monoclonal antibody by enzyme treatment, for example using papain to cleave the Fab portion from the Fc portion.

30 Preferably the antibody or derivative thereof is modified to make it less immunogenic in the patient. For example, if the patient is human the antibody may most preferably be 'humanised'; where the complimentarity determining region(s) of the hybridoma-derived antibody has been transplanted into a human monoclonal antibody, for example as described in Jones, P. et al., *Nature* 321:522-525 (1986), or Tempest et al., *Biotechnology* 9:266-273 (1991).

The modification need not be restricted to one of 'humanisation'; other primate sequences (for example Newman, R. *et al.*, Biotechnology 10:1455-1460 (1992)) may also be used.

5 The humanised monoclonal antibody, or its fragment having binding activity, form a particular aspect of this invention.

This invention provides a method of screening drugs to identify those which interfere with the proteins selected as targets herein, which method comprises measuring the interference of the activity of the protein by a test drug. For example if the protein selected has a catalytic activity, after suitable purification and formulation the activity of the enzyme 10 can be followed by its ability to convert its natural substrates. By incorporating different chemically synthesised test compounds or natural products into such an assay of enzymatic activity one is able to detect those additives which compete with the natural substrate or otherwise inhibit enzymatic activity.

15 The invention also relates to inhibitors identified thereby.

The use of a polynucleotide of the invention in genetic immunisation will preferably employ a suitable delivery method such as direct injection of plasmid DNA into muscles (Wolff *et al.*, Hum. Mol. Genet. 1:363 (1992); Manthorpe *et al.*, Hum. Gene Ther. 4:419 (1993)), delivery of DNA complexed with specific protein carriers (Wu *et al.*, J. Biol. Chem. 264:16985 (1989)), coprecipitation of DNA with calcium phosphate 20 (Benvenisty & Reshef, Proc. Nat'l Acad. Sci. USA 83:9551 (1986)), encapsulation of DNA in various forms of liposomes (Kaneda *et al.*, Science 243:375 (1989)), particle bombardment (Tang *et al.*, Nature 356:152 (1992)); Eisenbraun *et al.*, DNA Cell Biol. 12:791 (1993)) and *in vivo* infection using cloned retroviral vectors (Seeger *et al.*, Proc. Nat'l. Acad. Sci. USA 81:5849 (1984)). Suitable promoters for muscle transfection include 25 CMV, RSV, SRa, actin, MCK, alpha globin, adenovirus and dihydrofolate reductase.

In therapy or as a prophylactic, the active agent i.e., the polypeptide, polynucleotide or inhibitor of the invention, may be administered to a patient as an injectable composition, for example as a sterile aqueous dispersion, preferably isotonic.

30 Alternatively the composition may be formulated for topical application for example in the form of ointments, creams, lotions, eye ointments, eye drops, ear drops, mouthwash, impregnated dressings and sutures and aerosols, and may contain appropriate conventional additives, including, for example, preservatives, solvents to assist drug penetration, and emollients in ointments and creams. Such topical formulations may also contain compatible conventional carriers, for example cream or ointment bases, and ethanol

or oleyl alcohol for lotions. Such carriers may constitute from about 1% to about 98% by weight of the formulation; more usually they will constitute up to about 80% by weight of the formulation.

For administration to human patients, it is expected that the daily dosage level of 5 the active agent will be from 0.01 to 10 mg/kg, typically around 1 mg/kg. The physician in any event will determine the actual dosage which will be most suitable for an individual patient and will vary with the age, weight and response of the particular patient. The above dosages are exemplary of the average case. There can, of course, be individual instances where higher or lower dosage ranges are merited, and such are within the scope of this 10 invention.

A vaccine composition is conveniently in injectable form. Conventional adjuvants may be employed to enhance the immune response.

A suitable unit dose for vaccination is 0.5-5 µg/kg of antigen, and such dose is preferably administered 1-3 times and with an interval of 1-3 weeks.

15 Within the indicated dosage range, no adverse toxicological effects are expected with the compounds of the invention which would preclude their administration to suitable patients.

In order to facilitate understanding of the following example certain frequently occurring methods and/or terms will be described.

20 "Plasmids" are designated by a lower case p preceded and/or followed by capital letters and/or numbers. The starting plasmids herein are either commercially available, publicly available on an unrestricted basis, or can be constructed from available plasmids in accord with published procedures. In addition, equivalent plasmids to those described are known in the art and will be apparent to the ordinarily skilled artisan.

25 "Digestion" of DNA refers to catalytic cleavage of the DNA with a restriction enzyme that acts only at certain sequences in the DNA. The various restriction enzymes used herein are commercially available and their reaction conditions, cofactors and other requirements were used as would be known to the ordinarily skilled artisan. For analytical purposes, typically 1 µg of plasmid or DNA fragment is used with about 2 units of enzyme 30 in about 20 µl of buffer solution. For the purpose of isolating DNA fragments for plasmid construction, typically 5 to 50 µg of DNA are digested with 20 to 250 units of enzyme in a larger volume. Appropriate buffers and substrate amounts for particular restriction enzymes are specified by the manufacturer. Incubation times of about 1 hour at 37° C are ordinarily

used, but may vary in accordance with the supplier's instructions. After digestion the reaction is electrophoresed directly on a polyacrylamide gel to isolate the desired fragment.

Size separation of the cleaved fragments is performed using 8 percent polyacrylamide gel described by Goeddel, D. *et al.*, (1980) Nucleic Acids Res., 8:4057.

5 "Oligonucleotides" refers to either a single stranded polydeoxynucleotide or two complementary polydeoxynucleotide strands which may be chemically synthesized. Such synthetic oligonucleotides have no 5' phosphate and thus will not ligate to another oligonucleotide without adding a phosphate with an ATP in the presence of a kinase. A synthetic oligonucleotide will ligate to a fragment that has not been dephosphorylated.

10 "Ligation" refers to the process of forming phosphodiester bonds between two double stranded nucleic acid fragments (Maniatis, T., *et al.*, supra, p. 146). Unless otherwise provided, ligation may be accomplished using known buffers and conditions with 10 units to T4 DNA ligase ("ligase") per 0.5 µg of approximately equimolar amounts of the DNA fragments to be ligated.

15 **Example 1**

Isolation of DNA coding for a virulence gene in *Streptococcus pneumoniae*

As mentioned above each of the DNAs disclosed herein by virtue of the fact that it includes an intact open reading frame is useful to a greater or lesser extent as a screen for identifying antimicrobial compounds. A useful approach for selecting the preferred DNA sequences for screen development is evaluation by insertion-duplication mutagenesis. This system disclosed by Morrison *et al.*, J. Bacteriol. 159:870 (1984), is applied as follows.

Briefly, random fragments of *Streptococcus pneumoniae*, strain 0100993 DNA are generated enzymatically (by restriction endonuclease digestion) or physically (by sonication based shearing) followed by gel fractionation and end repair employing T4 DNA polymerase. It is preferred that the DNA fragments so produced are in the range of 200-400 base pairs, a size sufficient to ensure homologous recombination and to insure a representative library in *E.coli*. The fragments are then inserted into appropriately tagged plasmids as described in Hensel *et al.*, Science 269: 400-403(1995). Although a number of plasmids can be used for this purpose, a particularly useful plasmid is pJDC9 described by Pearce *et al.*, Mol. Microbiol. 9:1037 (1993) which carries the erm gene facilitating erythromycin selection in either *E. coli* or *S. pneumoniae* previously modified by incorporation of DNA sequence tags into one of the polylinker cloning sites. The tagged plasmids are introduced into the appropriate *S. pneumoniae* strain selected, inter alia, on the basis of serotype and virulence in a murine model of pneumococcal pneumonia.

It is appreciated that a seventeen amino acid competence factor exists (Havastein et al., *Proc. Nat'l. Acad. Sci. USA* 92:11140-44 (1995)) and may be usefully employed in this protocol to increase the transformation frequencies. A proportion of transformants are analysed to verify homologous integration and as a check on stability. Unwanted levels of reversion are minimized because the duplicated regions will be short (200-400 bp), however if significant reversion rates are encountered they may be modulated by maintaining antibiotic selection during the growth of the transformants in culture and/or during growth in the animal.

The *S. pneumoniae* transformants are pooled for inoculation into mice, e.g., Swiss and/or C57B1/6. Preliminary experiments are conducted to establish the optimum complexity of the pools and level of inoculum. A particularly useful model has been described by Veber et al. (*J. Antimicrobiol. Chemother.* 32:432 (1993) in which 10^5 cfu inocula sizes are introduced by mouth to the trachea. Strain differences are observed with respect to onset of disease e.g., 3-4 days for Swiss mice and 8-10 days for C57B1/6.

Infection yields in the lungs approach 10^8 cfu/lung. IP administration is also possible when genes mediating blood stream infection are evaluated. Following optimization of parameters of the infection model, the mutant bank normally comprising several thousand strains is subjected to the virulence test. Mutants with attenuated virulence are identified by hybridization analysis using the labelled tags from the "input" and "recovered" pools as probes as described in Hensel et al., *Science* 269: 400-403(1995). *S. pneumoniae* DNA is colony blotted or dot blotted, DNA flanking the integrated plasmid is cloned by plasmid rescue in *E. coli* (Morrison et al., *J. Bacteriol.* 159:870 (1984)) and sequenced. Following sequencing, the DNA is compared to the nucleotide sequences given herein and the appropriate ORF is identified and function confirmed for example by knock-out studies.

Expression vectors providing the selected protein are prepared and the protein is configured in an appropriate screen for the identification of anti-microbial agents. Alternatively, genomic DNA libraries are probed with restriction fragments flanking the integrated plasmid to isolate full-length cloned virulence genes whose function can be confirmed by "knock-out" studies or other methods, which are then expressed and incorporated into a screen as described above.

The individual full length sequences given herein are summarized in the following Tables (Table 1 and Table 2). Under the column in Table 1 labeled "Identity" there is the deduced identity of each open reading frame of the invention determined using Blastp and/or MPSearch. The ORF# column indicates whether the polynucleotide encoding each

ORF encodes more than one ORF. For example, SEQ ID NO:224 has an ORF# 1 but no #2; thus the polynucleotide encodes this ORF#1, but no other ORF was detected. On the other hand, SEQ ID NO:225 and 226 have ORF#s 1 and 2 respectively, indicating that they were both encoded by the same polynucleotide. This can also be seen in Table 2 where the 5 polynucleotide of SEQ ID NO: 2 encodes the ORFs of SEQ ID NOS: 225 and 226. Table 1 also shows the start ("START" column) and stop ("STOP" column) codons for each ORF and their positions in the encoding polynucleotide sequence. The SEQ ID NOS of the polypeptides of this table are linked to both a deduced identity in this table and a 10 polynucleotide sequence in Table 2 which encodes each polypeptide. The "Direction" column in Table 1 shows the direction of the ORF encoding each polypeptide in this table. "Forward" denotes the sense orientation and "Reverse" denotes the antisense orientation of the ORF.

TABLE 1

SEQ ID NO:	Identity	ORF #	Codon	Position	Start	Stop	Direction
224.	Phosphate Transport ATP-Binding Protein PSTB. - Escherichia	1	-CAT	TCA-	2	553	Reverse
225.	probable ATP binding protein - Bacillus subtilis	1	-CAT	TCA-	38	781	Reverse
226.	Nopaline Transport System Permease Protein Nocm. - Agrobacterium tumefaciens	2	-CAG	TTA-	781	1512	Reverse
227.	Aspartate Aminotransferase A (EC 2.6.11) (Transaminase A) (ASPAT.) - Rhizobium Meliloti.	1	ATG	TAG	480	671	Forward
228.	ISL2 protein - Lactobacillus helveticus	1	ATG	TAA	549	947	Forward
229.	ISL2 protein - Lactobacillus helveticus	2	ATG	TAG	889	1353	Forward
230.	Unknown	3	ATG	TGA	1421	1570	Forward
231.	Unknown	2	-CAT	CTA-	111	413	Reverse
232.	Unknown	11	ATG	TGA	133	282	Forward
233.	Acyl Carrier Protein (ACP.) - Rhizobium Meliloti.	1	-CAT	CTA-	673	906	Reverse
234.	Unknown	1	-CAT	TTA-	15	137	Reverse
235.	Unknown	2	-CAT	CTA-	681	989	Reverse
236.	Sulfate Transport System Permease Protein CYST (Fragment). - Synechocystis SP. (Strain PCC 6803).	2	-CAT	TTA-	336	689	Reverse
237.	probable transposase (insertion sequence IS861) - Streptococcus agalactiae (strain COH-1)	2	-CAT	TCA-	149	454	Reverse
238.	Unknown	2	-CAG	TTA-	567	851	Reverse
239.	"PTS SYSTEM	1	ATG	TAA	49	477	Forward
240.	"PTS SYSTEM	2	-CAT	TTA-	151	789	Reverse
241.	nitrogen fixation protein (nifS) homolog - Haemophilus influenzae (strain Rd KW 20)	1	-CAT	TCA-	1	207	Reverse
242.	cellobiose phosphotransferase system celA - Bacillus stearothermophilus	1	-CAT	TCA-	84	431	Reverse
243.	surface protein PspA - Streptococcus pneumoniae	1	ATG	TAA	22	321	Forward
244.	Unknown	2	ATG	TTAA	272	469	Forward
245.	ATP-dependent Clp proteinase (EC 3.4.21.-) chain clpL - Lactococcus lactis subs p. lactis	1	ATG	TGA	83	760	Forward

	plasmid pUCL22							
246.	Beta-Glucosidase (EC3.2.1.21) (Gentiobiase) (Cellobiase) (Beta-D-Glucoside GL Ucohydrolase) (Amygdalase). - <i>Bacillus Subtilis</i> .	1	-CAT	TCA-	153	599	Reverse	
247.	Glycine Betaine/L-Proline Transport ATP - Binding Protein Prov. - <i>Escherichia Col. I.</i>	2	ATG	TAA	159	887	Forward	
248.	Unknown	3	-CAT	TTA-	1102	1254	Reverse	
249.	30S Ribosomal Protein S11 (BS11). - <i>Bacillus Subtilis</i> .	1	ATG	TGA	15	164	Forward	
250.	DNA - Directed RNA Polymerase Alpha Chain (EC 2.7.7.6) (Transcriptase Alpha Chain). - <i>Bacillus Subtilis</i> .	2	ATG	TAA	282	1217	Forward	
251.	Peptide Chain Release Factor 3 (RF-3). - <i>Bacteroides Nodosus</i> (<i>Dichelobacter Nod Osus</i>).	1	ATG	TAG	212	667	Forward	
252.	Unknown	1	ATG	TAG	267	353	Forward	
253.	Riboflavin Synthase Alpha Chain (EC 2.5.1.9). - <i>Bacillus Subtilis</i> .	2	-CAT	CTA-	213	662	Reverse	
254.	Unknown	3	-CAT	TTA-	833	1045	Reverse	
255.	Unknown	1	-CAT	TTA-	83	424	Reverse	
256.	mesI protein - <i>Leuconostoc mesenteroides</i>	2	ATG	TAG	448	1302	Forward	
257.	Transacetylase BMTD (EC 2.3.1.-). - <i>Bacillus Subtilis</i> .	1	CTG	TAG	3	320	Forward	

SEQ ID NO:	Identity	ORF #	Codon	Position			
			Start	Stop	Start	Stop	Direction
258.	ribose-phosphate pyrophosphokinase (EC 2.7.6.1.) - <i>Bacillus caldolvticus</i>	1	CTG	TAG	1	642	Forward
259.	Unknown	1	ATG	TAA	66	614	Forward
260.	Unknown	1	ATG	TAG	108	590	Forward
261.	nitrogenase C (nifC) homolog - <i>Haemophilus influenzae</i> (strain Rd KW20)	2	ATG	TAG	631	855	Forward
262.	Unkown	2	ATG	TAA	606	752	Forward
263.	Unknown	2	ATG	TGA	280	495	Forward
264.	Unknown	2	ATG	TGA	639	1466	Forward
265.	Acetyl Esterase (EC 3.1.---) - <i>Caldocellum Saccharolvticum</i> .	2	ATG	TAA	274	594	Forward
266.	Unknown	1	-CAT	TCA-	2	157	Reverse
267.	Triosephosphate Isomerase (EC 5.3.1.1) (TIM) - <i>Bacillus Subtilis</i> .	1	-CAT	TTA-	270	665	Reverse
268.	Branched-chain Amino Acid Aminotransferase (EC 2.6.1.42) (Transaminase B) - <i>Escherichia Coli</i> .	1	ATG	TAG	110	736	Forward
269.	branched-chain-amino-acid transaminase homolog - <i>Haemophilus influenzae</i> (strain Rd KW20)	2	ATG	TAA	708	842	Forward
270.	DnaK protein - <i>Lactococcus lactis</i>	1	CTG	TGA	3	749	Forward
271.	Ketol-Acid Reductoisomerase (EC 1.1.1.86) (Acetohydroxy-Acid Isomero-reductase) - <i>Lactococcus Lactis</i> (Subsp. <i>Lactis</i>) (<i>Streptococcus Lactis</i>)	1	ATG	TAA	99	428	Forward
272.	Unknown	1	-CAT	CTA-	278	631	Reverse
273.	Amidophosphoribosyltransferase Precursor (EC 2.4.2.14) (Glutamine Phosphoribosyl Pyrophosphate Amidotransferase) (Atase) - <i>Bacillus Subtilis</i> .	2	-CAT	CTA-	152	775	Reverse
274.	Pyrrolidone-Carboxylate Peptidase (EC 3.4.19.3) (5-Oxoprolyl-Peptidase) - <i>STR Epococcus Pvogenes</i> .	1	-CAT	TCA-	156	803	Reverse
275.	50S Ribosomal Protein L16. - <i>Mycoplasma Capricolum</i> .	1	ATG	TAA	33	416	Forward
276.	serine O-acetyltransferase (EC 2.3.1.30) - <i>Bacillus stearothermophilus</i>	2	-CAT	CTA-	577	1194	Reverse
277.	Unknown	1	ATG	TAG	61	648	Forward

278.	Unknown	1	-CAT	CTA-	165	335	Reverse
279.	Lipoprotein Signal Peptidase (EC 3.4.23.36) (Prolipoprotein Signal Peptidase) (Signal Peptidase II) (Spase II). - <i>Staphylococcus Aureus</i> .	1	ATG	TAA	56	517	Forward
280.	Unknown	1	ATG	TAA	214	534	Forward
281.	Alpha-Acetylactate Decarboxylase (EC 4.1.1.5). - <i>Bacillus Subtilis</i> .	1	-CAT	CTA-	104	445	Reverse
282.	Dihydrodipicolinate Synthase 9 (EC 4.2.1.52) (DHDPS). - <i>Bacillus Subtilis</i> .	3	-CAT	TCA-	675	884	Reverse
283.	Polyribonucleotide Nucleotidyltransferase (EC 2.7.7.8) (Polynucleotide Phosphorylase) (Pnpase). - <i>Photorhabdus Luminescens</i> .	1	-CAT	TCA-	1	855	Reverse
284.	Single-Strand Binding Protein (SSB) (Helix-Destabilizing Protein). - <i>Bacillus S Ubtillis</i>	1	-CAT	TTA-	128	598	Reverse
285.	ATP-Dependent CLP Protease ATO-Binding Subunit CLPX. - <i>Escherichia Coli</i> .	2	-CAT	CTA-	195	482	Reverse
286.	ATP-Dependent CLP Protease ATO-Binding Subunit CLPX. - <i>Escherichia Coli</i>	4	-CAG	TCA-	676	990	Reverse
287.	N-(5'-Phosphoribosyl) Anthranilate Isomerase (EC 5.3.1.24) (PRAI). - <i>Lactococcus Lactis</i> (Subsp. <i>Lactis</i>) (<i>Streptococcus Lactis</i>).	1	ATG	TAA	83	712	Forward
288.	30S Ribosomal Protein S2. - <i>Escherichia Coli</i> .	1	ATG	TGA	277	591	Forward
289.	30S Ribosomal Protein S2. - <i>Escherichia Coli</i> .	3	ATG	TGA	918	1064	Forward
290.	Possible beta-galactosidase precursor	1	-CAT	CTA-	120	545	Reverse
291.	Unknown	1	-CAT	TTA-	77	283	Reverse
292.	Unknown	1	-CAT	TTA-	1	198	Reverse
293.	"Phospho-2-Dehydro-3-Deoxyheptonate Aldolase	1	-CAT	TTA-	217	690	Reverse

SEQ ID NO:	Identity	ORF #	Codon	Position			
			Start	Stop	Start	Stop	Direction
294.	Unknown	2	-CAT	TTA-	429	599	Reverse
295.	Unknown	3	-CAT	TCA-	739	936	Reverse
296.	Sorbitol Dehydrogenase (EC 1.1.1.14) (L-Iditol 2-Dehydrogenase). - <i>Bacillus Subtilis</i> .	1	ATG	TAA	64	480	Forward
297.	EBG Operon Repressor. - <i>Escherichia Coli</i> .	2	-CAT	CTA-	668	1060	Reverse
298.	cellobiose phosphotransferase system celA - <i>Bacillus stearothermophilus</i>	2	-CAT	TTA-	249	566	Reverse
299.	Unknown	3	-CAT	TCA-	581	964	Reverse
300.	Adenylosuccinate Lyase (EC 4.3.2.2) (Adenylosuccinase) (ASL). - <i>Bacillus Subtilis</i> .	1	-CAT	TTA-	99	809	Reverse
301.	ATP-Binding Protein BEXA. - <i>Haemophilus Influenzae</i> .	1	ATG	TGA	111	404	Forward
302.	L-Lactate Dehydrogenase (Cytochrome) (EC 1.1.2.3). - <i>Escherichia Coli</i> .	2	ATG	TAA	337	507	Forward
303.	Phosphate Transport System Permease Protein PSTC. - <i>Escherichia Coli</i> .	3	ATG	TGA	507	1070	Forward
304.	Sulfate Transport ATP-Binding Protein Cysa. - <i>Synechococcus SP. (Strain PCC 7942) (Anacystis Nidulans R2)</i> .	1	-CAT	CTA-	110	838	Reverse
305.	Unknown	2	-CAT	TTA-	838	1077	Reverse
306.	Unknown	2	-CAT	TCA-	282	749	Reverse
307.	Unknown	2	ATG	TAG	1108	1290	Forward
308.	Phosphoribosylformylglycinamide Cyclo-Ligase (EC 6.3.3.1) (AIRS) (Phosphoribosyl-Aminoimidazole Synthetase) (AIR Synthase). - <i>Bacillus Subtilis</i> .	2	-CAT	TCA-	331	477	Reverse
309.	Unknown	2	ATG	TAA	313	765	Forward
310.	SMS Protein. - <i>Escherichia Coli</i> .	1	-CAT	TCA-	102	416	Reverse
311.	sigma 42 protein - <i>Enterococcus faecalis</i>	1	-CAT	TCA-	8	487	Reverse
312.	Unknown	1	-CAT	TTA-	76	390	Reverse
313.	Guanylate Kinase (EC 2.7.4.8) (GMP Kinase). - <i>Escherichia Coli</i> .	2	-CAG	TTA-	415	849	Reverse
314.	Unknown	1	-CAT	TCA-	51	296	Reverse
315.	Unknown	1	ATG	TAA	175	285	Forward
316.	Unknown	2	ATG	TAA	361	558	Forward
317.	Unknown	3	ATG	TAA	383	1144	Forward

318.	"PTS System	2	-CAT	TCA-	166	465	Reverse
319.	L-Fucose Isomerase (EC 5.3.1.-) - Escherichia Coli.	1	-CAT	CTA-	9	482	Reverse
320.	Unknown	2	-CAT	TTA-	495	650	Reverse
321.	Unknown	1	ATG	TGA	130	231	Forward
322.	3-Oxoacyl-[Acyl-Carrier Protein] Reductase (EC 1.1.1.100) (3-Ketoacyl- Acyl Carrier Protein Reductase). - Escherichia Coli.	1	-CAT	TCA-	51	200	Reverse
323.	3-Oxoacyl-[Acyl-Carrier Protein] Reductase (EC 1.1.1.100) (3-Ketoacyl- Acyl Carrier Protein Reductase). - Escherichia Coli.	2	-CAT	TCA-	231	614	Reverse
324.	2-Isopropylmalate Synthase (EC 4.1.3.12) (Alpha-Isopropylmalate Synthase) (Alph A-IPM Synthetase). - Lactococcus Lactis (Subsp. Lactis) (Streptococcus Lactis).	1	-CAT	TTA-	31	231	Reverse
325.	2-Isopropylmalate Synthase (EC 4.1.3.12) (Alpha-Isopropylmalate Synthase) (Alph A-IPM Synthetase). - Lactococcus Lactis (Subsp. Lactis) (Streptococcus Lactis).	2	-CAT	TCA-	191	334	Reverse
326.	Unknown	3	-CAT	TCA-	309	452	Reverse
327.	2-Isopropylmalate Synthase (EC 4.1.3.12) (Alpha-Isopropylmalate Synthase) (Alph A-IPM Synthetase). - Lactococcus Lactis (Subsp. Lactis) (Streptococcus Lactis).	4	-CAT	TTA-	495	1127	Reverse
328.	Unknown	2	-CAT	TCA-	170	469	Reverse
329.	Unknown	1	ATG	TAG	105	473	Forward
330.	Strscaa Ncbi gi: 310629NCBI gi: 473 - Streptococcus gordoni (strain PK488) DNA	1	-CAG	CTA-	81	665	Reverse

SEQ ID NO:	Identity	ORF #	Codon	Position			
			Start	Stop	Start	Stop	Direction
331.	Unknown	1	ATG	TGA	228	374	Forward
332.	lysyl aminopeptidase (EC 3.4.11.15) precursor - Lactococcus lactis	1	-CAT	TCA-	107	766	Reverse
333.	Indole-3-Glycerol Phosphate Synthase (EC 4.1.1.48) (IGPS). - Lactococcus Lactis (SUBSP. Lactis) (Streptococcus Lactis)	1	-CAT	TCA-	127	369	Reverse
334.	Anthraniate Phosphoribosyltransferase (EC 2.4.2.18). - Lactococcus Lactis (Sub SP. Lactis) (Streptococcus Lactis).	2	-CAA	TCA-	366	641	Reverse
335.	Tagatose-6-Phosphate Kinase (EC 2.7.1.-) (Phosphotagatokinase). - Lactococcus Lactis (Subsp. Lactis) (Streptococcus Lactis)	1	ATG	TGA	42	524	Forward
336.	Unknown	1	ATG	TGA	73	474	Forward
337.	Unknown	1	-CAT	TTA-	32	286	Reverse
338.	Unknown	1	ATG	TGA	306	572	Forward
339.	Acetylactate Synthase Large Subunit (EC 4.1.3.18) (AHAS) (Acetylhydroxy-Acid Synthase Large Subunit) (ALS). - Lactococcus Lactis (SUBSP. Lactis) (Streptococcus Lactis).	1	ATG	TAG	59	502	Forward
340.	Penicillin-Binding Proteins 1A/1B. - Bacillus Subtilis.	2	ATG	TGA	535	720	Forward
341.	Unknown	1	ATG	TAG	165	488	Forward
342.	Anthraniate Phosphoribosyltransferase (EC 2.4.2.18). - Lactococcus Lactis (SUB SP. Lactis) (Streptococcus Lactis).	1	-CAT	TCA-	5	394	Reverse
343.	grpE protein - Lactococcus Lactis	2	ATG	TAA	124	543	Forward
344.	Unknown	1	-CAT	CTA-	34	195	Reverse
345.	Unknown	2	-CAT	TTA-	377	544	Reverse
346.	Unknown	2	ATG	TAA	159	503	Forward
347.	Unknown	2	-CAT	CTA-	315	644	Reverse
348.	Unknown	2	-CAT	CTA-	468	587	Reverse
349.	Unknown	2	-CAT	CTA-	482	631	Reverse
350.	Unknown	2	-CAT	TTA-	380	757	Reverse
351.	NIFS Protein Homolog (Fragment). - Lactobacillus Delbrueckii (SUBSP. Bulgaricus).	1	ATG	TAG	87	797	Forward
352.	"Ornithine Carbamoyltransferase	1	TTG	TAA	2	502	Forward

353.	PSEG LI NCBI gi: 499660 - Pseudomonase putida.	1	-CAT	TTA-	50	481	Reverse
354.	Unknown	1	CTG	TAA	1	522	Forward
355.	Thioredoxin. - Streptomyces Clavuligerus.	1	ATG	TAG	58	375	Forward
356.	D-alanine permease (dagA) homolog - Haemophilus influenzae (strain Rd KW20)	1	ATG	TAG	185	343	Forward
357.	Unknown	1	-CAT	TTA-	78	371	Reverse
358.	"DNA Polymerase III	1	-CAA	TCA-	82	561	Reverse
359.	Transport ATP-Binding Protein ComA. - Streptococcus Pneumoniae.	1	-CAT	TTA-	112	552	Reverse
360.	Unknown	2	ATG	TAA	445	540	Forward
361.	surface protein PspA - Streptococcus pneumoniae	1	-CAT	TCA-	45	416	Reverse
362.	Licid Protein. - Haemophilus influenzae	2	ATG	TAA	268	633	Forward
363.	Unknown	2	ATG	TAA	527	640	Forward
364.	Glutamine Transport ATP- Binding Protein GLNQ. - Escherichia Coli.	1	CTG	TGA	1	393	Forward
365.	Unknown	1	ATG	TAG	184	303	Forward
366.	Unknown	1	ATG	TGA	794	919	Forward
367.	Lipoamide Dehydrogenase Component (E3) of Pyruvate Dehydrogenase Complex (EC 1.8.1.4) (Dihydrolipoamide Dehydrogenase). - Azotobacter Vinelandii.	1	ATG	TAA	3	416	Forward

SEQ ID NO:	Identity	ORF #	Codon	Position			
			Start	Stop	Start	Stop	Direction
368.	Orotate Phosphoribosyltransferase (EC 2.4.2.10) (OPRT). - <i>Bacillus Subtilis</i> .	1	-CAT	CTA-	21	311	Reverse
369.	Unknown	1	ATG	TAA	28	309	Forward
370.	SPOOB-Associated GTP-Binding Protein. - <i>Bacillus Subtilis</i> .	1	ATG	TGA	110	538	Forward
371.	Transport ATP-Binding Protein COMA. - <i>Streptococcus Pneumoniae</i> .	1	-CAA	TCA-	47	679	Reverse
372.	prephenate dehydrogenase (EC 1.3.1.12) - <i>Lactococcus lactis</i> .	2	ATG	TAG	271	492	Forward
373.	O-Sialoglycoprotein Endopeptidase (EC 3.4.24.57) (Glycoprotease). - <i>Pasteurella Haemolytica</i> .	1	CTG	TAA	1	450	Forward
374.	Unknown	1	-CAT	TTA-	7	282	Reverse
375.	Unknown	1	TTG	TAA	2	265	Forward
376.	"DNA Polymerase III	1	ATG	TGA	3	401	Forward
377.	Unknown	2	ATG	TAA	361	516	Forward
378.	Dihydrodipicolinate Synthase (EC 4.2.1.52) (DHDPS). - <i>Bacillus Subtilis</i> .	1	-CAT	TTA-	179	457	Reverse
379.	Unknown	2	-CAT	TCA-	104	322	Reverse
380.	Unknown	2	-CAT	TCA-	248	649	Reverse
381.	Unknown	1	-CAT	TTA-	56	394	Reverse
382.	Unknown	2	-CAT	TTA-	254	409	Reverse
383.	Unknown	1	ATG	TAG	138	617	Forward
384.	Unknown	2	-CAT	TTA-	225	479	Reverse
385.	Unknown	2	ATG	TAA	747	857	Forward
386.	Unknown	1	ATG	TAG	294	443	Forward
387.	Unknown	2	ATG	TGA	356	544	Forward
388.	Unknown	1	-CAT	CTA-	4	141	Reverse
389.	Unknown	1	CTG	TAG	1	579	Forward
390.	Unknown	2	-CAT	TTA-	309	452	Reverse
391.	Phosphopentomutase (EC 5.4.2.7). - <i>Escherichia Coli</i> .	1	ATG	TAA	3	233	Forward
392.	D-Alanyl-D-Alanine Carboxypeptidase Precursor (EC 3.4.16.4) (DD-Peptidase)(DD-Carboxypeptidase)(Cpase)(PBP5). - <i>Bacillus Subtilis</i> .	1	-CAT	TTA-	52	537	Reverse
393.	Na+ and Cl-dependent gamma-aminobutyric acid transporter homolog-Haemophilus	1	TTG	TGA	2	268	Forward

	<i>influenzae</i> (strain Rd KW20)						
394.	Unknown	2	ATG	TGA	319	546	Forward
395.	dihydrolipoamide dehydrogenase (EC 1.8.1.4) - <i>Pelobacter carbinolicus</i>	1	ATG	TGA	3	284	Forward
396.	Unknown	2	ATG	TGA	241	450	Forward
397.	Beta-Glucosidase A (EC 3.2.1.21)(Gentiobiase)(Cellobiase)(Beta-D-Glucoside Glucohydrolase). - <i>Clostridium Thermocellum</i> .	1	ATG	TAA	184	453	Forward
398.	Uracil Permease. - <i>Bacillus Caldolyticus</i> .	1	ATG	TAA	93	353	Forward
399.	Unknown	2	ATG	TAG	127	516	Forward
400.	Ligoendopeptidase F- <i>Lactococcus lactis</i>	1	ATG	TGA	134	310	Forward
401.	Strepasea NCBI gi: 153565NCBI gi: 4- <i>Streptococcus Faecalis</i> DNA.	2	ATG	TAA	392	568	Forward
402.	Unknown	2	ATG	TAA	376	507	Forward
403.	Exodeoxyribonuclease Small Subunit (EC 3.1.11.6) (Exonuclease VII Small Subunit). - <i>Escherichia Coli</i> .	2	-CAT	TCA-	470	682	Reverse
404.	ATP-Dependent DNA Helicase RECG (EC 3.6.1.-). - <i>Escherichia Coli</i> .	1	ATG	TGA	3	455	Forward

SEQ ID NO:	Identity	ORF #	Codon	Position			
			Start	Stop	Start	Stop	Direction
405.	Possible thiamin biosynthetic enzyme	1	-CAT	TTA-	15	347	Reverse
406.	SPOU Protein. - Escherichia Coli.	2	ATG	TAA	322	618	Forward
407.	Malonyl Coa-Acyl Carrier Protein Transacylase (EC 2.3.1.39). - Escherichia Coli.	1	ATG	TAG	85	498	Forward
408.	Unknown	1	-CAT	CTA-	17	118	Reverse
409.	nucleoside diphosphate kinase (ndk) homolog- Haemophilus influenzae (strain Rd KW20)	1	CTG	TGA	1	159	Forward
410.	Nucleoside Diphosphate Kinase (EC 2.7.4.6)(NDK) (NDP Kinase). - Escherichia Co L1.	2	ATG	TAG	215	481	Forward
411.	Unknown	1	-CAT	TTA-	21	368	Reverse
412.	Unknown	2	-CAT	TCA-	162	314	Reverse
413.	Unknown	1	ATG	TAA	187	417	Forward
414.	Unknown	2	ATG	TGA	316	417	Forward
415.	Unknown	1	ATG	TGA	316	453	Forward
416.	Enolase (EC 4.2.1.11)(2-Phosphoglycerate Dehydratase)(2-Phospho-DGlycerate Hydro-Lvase). - Bacillus Subtilis.	1	-CAT	TTA-	4	435	Reverse
417.	Unknown	1	CTG	TGA	1	363	Forward
418.	Unknown	1	ATG	TGA	39	383	Forward
419.	PILB Protein. - Neisseria Gonorrhoeae.	1	-CAT	TTA-	145	327	Reverse
420.	Unknown	2	ATG	TGA	285	533	Forward
421.	Unknown	1	CTG	TAG	2	379	Forward
422.	integrase/recombinase (xprB) homolog - Haemophilus influenzae (strain Rd KW20)	1	ATG	TAA	305	421	Forward
423.	Unknown	1	-CAT	CTA-	173	436	Reverse
424.	Unknown	1	-CAT	CTA-	182	427	Reverse
425.	Unknown	1	ATG	TAA	49	372	Forward
426.	"Mutator Mutt Protein (7	1	-CAT	CTA-	21	446	Reverse
427.	Unknown	1	ATG	TGA	177	380	Forward
428.	Possible phosphatase	1	ATG	TAG	112	402	Forward
429.	Unknown	1	ATG	TGA	110	271	Forward
430.	Phosphoenolpyruvate Carboxylase (EC 4.1.1.31). - Corynebacterium Glutamicum.	2	ATG	TGA	337	561	Forward
431.	Unknown	1	ATG	TGA	214	324	Forward
432.	50S Ribosomal Protein L31. - Bacillus	1	ATG	TAA	142	426	Forward

	Subtilis						
433.	glycosyl transferase (lgtD) homolog - <i>Haemophilus influenzae</i> (strain Rd KW20)	1	ATG	TGA	127	399	Forward
434.	Unknown	2	-CAT	CTA-	244	435	Reverse
435.	Unknown	2	ATG	TGA	118	309	Forward
436.	Factor essential for Expression of Methicillin Resistance. - <i>Staphylococcus Aur Eus.</i>	2	-CAT	TTA-	168	434	Reverse
437.	Unknown	1	-CAT	TCA-	2	214	Reverse
438.	Unknown	1	TTG	TAA	2	142	Forward
439.	Unknown	1	ATG	TAA	30	191	Forward

SEQ ID NO:	Identity	ORF #	Codon		Position		Direction
			Start	Stop	Start	Stop	
440.	Aspartate Aminotransferase (EC 2.6.1.1) (Transaminase A)(ASPAT). - <i>Bacillus</i> SP. (STRAIN YM-2).	1	-CAT	TCA-	63	416	Reverse
441.	Unknown	1	ATG	TAA	52	342	Forward
442.	Unknown	2	-CAT	TCA-	210	455	Reverse
443.	Unknown	1	TTG	TGA	2	517	Forward
444.	ATP-Dependent DNA Helicase RECG (EC 3.6.1.-) - <i>Escherichia Coli</i> .	1	ATG	TGA	83	376	Forward
445.	Unknown	1	ATG	TAA	70	384	Forward
446.	Cell Division Protein FTSA. - <i>Bacillus Subtilis</i> .	1	TTG	TAA	3	371	Forward
447.	Unknown	1	ATG	TAG	70	441	Forward
448.	Unknown	1	ATG	TAG	104	454	Forward
449.	Unknown	1	CTG	TAA	1	159	Forward
450.	Unknown	1	ATG	TAA	120	347	Forward
451.	Unknown	1	ATG	TGA	31	423	Forward
452.	Unknown	2	ATG	TGA	225	416	Forward
453.	Unknown	1	ATG	TGA	290	418	Forward
454.	Unknown	1	ATG	TGA	3	269	Forward
455.	JAG Protein (SPOIJJ Associated Protein). - <i>Bacillus Subtilis</i> .	1	ATG	TGA	93	365	Forward
456.	"DNA -3-Methyladenine Glycosidase I (EC 3.2.2.20)(3-Methyladenine-DNA Glycosylase I	1	ATG	TAG	91	282	Forward
457.	"Glucan I	1	-CAT	TTA-	4	150	Reverse
458.	Unknown	1	-CAT	CTA-	245	400	Reverse
459.	Glutamate/Aspartate Transport ATP-Binding Protein GLTL. - <i>Escherichia Coli</i> .	1	-CAT	TCA-	81	218	Reverse
460.	Unknown	1	-CAT	TTA-	103	492	Reverse
461.	Unknown	1	ATG	TGA	305	484	Forward
462.	Unknown	1	-CAT	TCA-	29	355	Reverse
463.	Unknown	2	-CAT	TTA-	572	838	Reverse
464.	Unknown	2	-CAT	TCA-	652	1026	Reverse
465.	Unknown	2	-CAT	TTA-	318	764	Reverse
466.	Unknown	2	ATG	TGA	719	805	Forward
467.	Llcpqrda NCBI gi: 511014 - <i>Lactococcus lactis</i> .	1	ATG	TGA	134	472	Forward

468.	Unknown	1	ATG	TGA	385	492	Forward
469.	Unknown	2	ATG	TAA	587	721	Forward
470.	galE protein - Neisseria meningitidis	1	-CAT	TCA-	23	460	Reverse
471.	Unknown	2	-CAG	TTA-	717	1319	Reverse
472.	Naphthoate Synthase (EC 4.1.3.36) (Dihydroxynaphthoic Acid Synthetase)(Dhna Sy Nthetase). - Escherichia Coli.	1	ATG	TGA	97	414	Forward

SEQ ID NO:	Identity	Codon		Position		Direction
		ORF #	Start Stop	Start	Stop	
473.	Unknown	1	CTG	TGA	1	246 Forward
474.	Unknown	1	-CAT	TCA-	341	748 Reverse
475.	Unknown	1	-CAT	TTA-	217	858 Reverse
476.	Unknown	1	-CAT	TTA-	499	729 Reverse
477.	Multiple Sugar-Binding Transport ATP-Binding Protein MSMK. - Streptococcus MUTA NS.	2	ATG	TAA	407	571 Forward

Table 2 shows the correlation between the SEQ ID NO of each DNA sequence of the invention with the SEQ ID NO(S) of polypeptide or polypeptides that its open reading frame(s) encodes. For example, the DNA of SEQ ID NO:1 encodes one polypeptide, that of SEQ ID NO:224. Whereas, the DNA of SEQ ID NO:2 encodes two polypeptides, the polypeptides of SEQ ID NO:225 and SEQ ID NO:226.

TABLE 2

DNA	Protein (open reading frame)
1	224
2	225,226
3	227
4	228,229,230
5	231
6	232
7	233
8	234
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10	236
11	237
12	238
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17	243,244
18	245
19	246
20	247,248
21	249,250
22	251
23	252
24	253,254
25	255,256
26	257
27	258
28	259
29	260,261
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31	263
32	264
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35	267
36	268,269
37	270
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42	275
43	276
44	277
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52	285,286
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54	288,289
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64	302,303
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78	322,323
79	324,325,326,327
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85	333,334
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95	344,345
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214	466
215	467
216	468,469
217	470,471
218	472
219	473
220	474
221	475
222	476
223	477

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Black, Michael
Hodgson, John
Knowles, David
Nicholas, Richard
Stodola, Robert

(ii) TITLE OF THE INVENTION: Novel Compounds

(iii) NUMBER OF SEQUENCES: 477

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SmithKline Beecham Corporation
(B) STREET: 709 Swedeland Road
(C) CITY: King of Prussia
(D) STATE: PA
(E) COUNTRY: USA
(F) ZIP: 19406-0939

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 01-APR-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/014690
(B) FILING DATE: 02-APR-1996

PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/025788
(B) FILING DATE: 22-AUG-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Gimmi, Edward R
(B) REGISTRATION NUMBER: 38,891

(C) REFERENCE/DOCKET NUMBER: P50466

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 610-270-4478
- (B) TELEFAX: 610-270-5090
- (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 683 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCAAACATG	GTCTCTTCTA	GTTGCATGGT	CGCAATCGGA	TCCAAGGCTG	AGGCTGGGCT	60
CATCCATTAA	GAGGATATCT	GGCTTAACAG	AGATGGCACG	AGCGATAACAG	AGACGTTGTT	120
GCTGACCACC	TGATAAGGTC	AAGGCTGACT	TGTGGAGATC	GTCTTAAACC	TGATCCAAA	180
GGGCAGCCTG	ACTAAGGGAG	GTTTCTACGA	TTTCATCTAG	GACTTGCTTA	TCCTTAACTC	240
CAGCACGTTC	ATGCGCAAAG	GTAATATTAC	GGTAAATTGA	CTTAGCAAAT	GGATTGGGGC	300
GTTGAAAAAC	CATTCCAATG	TGTTTACGCA	TTTCATAAAC	GTTGATTCT	GGACGGTTGA	360
CATCAATTCC	ACGATAGAGA	ATCTGCCAG	TTACTTTAGC	AATATCAATG	GTATCATTCA	420
TGCGATTGAG	ACTGCCATAAG	TAGGTAGATT	TCCCCGATCC	CGACGGACCA	ATCAAAGCTG	480
TAATTTTATT	TCCTTCAAA	TTGCATATCA	ATCCCCCTAA	TGGATTCTT	TTTACCATAG	540
TAAACATGGA	CATCCTTAGT	AGAAAGGGCT	ACTTTTTCTT	CAGGAAAGGT	AAGGATATGC	600
TTCTCATCCC	AGTTATATGT	TGACATGGCT	TCTCCTTCTAG	GCAGCGGTTA	ATTCTTGTG	660
TAGATAGCTT	CCGAACCTAC	GAG				683

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTAGTCCAAC	TAACTGAGTT	TTCCTTTATC	TATTATATCA	AATATAAGTC	CGTTTGTAAC	60
TAGTGAAGAA	TTCTTTGTC	CGCTCTCTT	TAGGGGTGTG	GATAATCTCA	TCCGGAGTTC	120
CAGACTCGAT	GATTTCCCC	TTATCTAAGA	AGAGAATTT	ATCCGCAACT	TGGGCTACAA	180
AGGGCATGTC	ATGACTGACC	AAAATCATGG	TCTGACCTGA	CTTAGCAGCA	TCTGCAATAG	240
ACTTTCTAC	TTCACCGACC	AATTCTGGT	CAAGGGCTGA	AGTTGGTTCG	TCTAAGAGCA	300
AAACATCTGG	TTTCATAGCA	AGCGCACGCG	CTAGGGCAAC	CCGTTGCTTC	TGTCCACCTG	360
ATAAAATGGCG	AGGATAATGG	TTTCACGGT	CCGAAAGCCC	AACCTTAGCC	AACTCTTCT	420
TGGCAATCTT	AGTCGCTCT	TGGTCAGATA	ATTTCCTTGAC	AACAACCAAG	CCTTCTTCA	480
CATTATCAAG	TGCTGTTCGG	CGTTCAAATA	AATTAAACTG	TTGGAAAACC	ATAGACAAC	540
TACGGCGTAG	GGCAAGGATT	TCTTCTTGAG	TGATTTAGA	AAAATCAACT	GAAAAACCAT	600
CAATCTGAAT	AGAGCCACTG	TCAGGTGTTT	CAAGATAATT	GAGACTGCGA	AGAAAGGTTG	660
ATTTTCCAGC	TCCTGAAGAA	CCAATCAAGG	CTACAACCTTC	CCCTTTTGAA	ATATCCAAGT	720
TCAGATGATC	CAAGACAGTC	TGTCCTGAAA	AGGATTTGCT	TAAATCGAA	ATCTTAATCA	780
TTAACGAAGG	TCTCCTTCA	CATCTGTTG	CACTGTATCA	GGTGCAGAAA	TAGCCATT	840
TCTCTCGATG	AAACGACCGA	GGCTTCAAT	TCCGATATTG	ACTACCCAAT	AAACAAGGGC	900
AACAGAGATG	AAGCGTTCAA	AATAGCGATA	ATCAGCTCCA	CCTAGAAATCT	GAGCTTGGGC	960
AAAGACTTCC	ACAACACCCG	CACTAAAAGC	TAGAGATGTT	CCCTGGTCA	AACCGATGAG	1020
GGAATTAAATC	AAGGGTGGAG	TAGCTACCAAC	CGCTGCATTA	GGAATAATCA	CTCGTCGATA	1080
AACTTGCCT	CGGGTCATAC	CCAGACTGCG	CGCCGCCCTCA	ATCTCACCAG	GATTAAC	1140
GAGAATGGCT	GCACCGAATGG	TTTCACTAGC	ATAAGCTGCC	TCATTAAAGG	CAAAGCGAC	1200
AATCGCAAAA	GCTGCAGCTG	GAATCGCATT	GATATTGAGA	CCAGTTCCCC	ATTGCTGATT	1260
GAGGGCTTTC	AAAGCCAAAG	GGATTCCGTA	GTAGGTCAAC	ATGAGTTGCA	CCAAAATCGG	1320
TGTCCCTTT	AAGAAACTAA	CAAAGAAGGC	CTGCAAGGGA	TATAAAATCT	TGACACGATT	1380
GATCTTCACA	ATGGCAAAA	GAAGCGCCAA	AACCAAGCCA	AAAAGGGCAC	CGCCAATTGT	1440
CAACATAATT	GTTGTTGGAA	GTTGTTGGAC	AATTCTAGGG	ATTCCATCAA	AGACCGAACG	1500
TAGGCTAAAC	AG					1512

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 709 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTGGAGATTA	TTGAGATTGC	CCGTCAAAAC	GATTGATTA	TNTTTGCGGA	TGAAATCTAT	60
GACCGCATGG	TAAATGGACG	GACATGTGCA	TAACGCCCTGT	GGCGAGCTTG	GCACCCAGATG	120
TCTTCTGTGT	CAGCATGAAT	GGTCTGTCAA	AATCCCACCG	CATAGCAGGT	TTCCCGTGTG	180
GGATGGATGG	TCTTGTCTGG	CCCTAAGACT	CATGTTAAGG	GCTATATCGA	AGGGCTCAAT	240

ATGCTGTCCA ATATGCGCCT TTGCTCTAAC GTTTGCGCTA CCAACGCTGC ATTAGGAATA	300
ATCACTGTCG TACAAACTTG CGCTTGGGGG GTCACCAATC AGTCGATGAA TTGCTTCTTC	360
CTGGTGGACG AATCTACGAG CAAAGAAATT TCATCTATAA TGCCATTCAA GATATTCCAG	420
GTTTGTCTGC CGTAAACCC AAGGCGGGC TCTATATCTT CCCAAAAATC GACCGAATA	480
TGTACCGTAT CGATGATGAT GAGCAGTTG TCCTTGATTT CTTGAAGCAG GAAAAGGTTTC	540
TCTTGGTTCA TGGTCGAGGC TTTAACTGGC AGGAACCAGA CCACCTCCGT ATCGTTTACC	600
TTCCTCGTGT TGATGAGTTA GCCCAAATCC AAGAAAAGAT GACTCGTTTC TTGAAACAGT	660
ATCGTAGATA GGGCTTGCAT TCGAAAAAGC TGGAAACATT TGCCTAGAG	709

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CTGCTTCAGA ACCTGCCAAA CCAGCACCGA TAACATTGAT ATAAGATTGA GACACGACAC	60
TAATACCTCT TTGGGAGTGT GAAGTTAAGA TTCACATTGA AAAAGCCAAT CAGACTTACA	120
AGCTTTGAG TTTCTTGGCT CAGGCTGAAA AAGTCCACAG GGCTTTNCA CTCCCACAAA	180
TCTTTCTATT TTTTCTNCTA CTAGTATAAC AAAAAAAAGGG AAGAAGNAA ACTTCCCTGT	240
TTAGTCATTT TCTTGATGTA AAGAGATAGT GAGTATTCCA GTTAAGAATC AATTATATGC	300
TACTCTATAA AATCTTTCC ACATAACCGA TCGATAGGGA CTGTTATTCT ATCTCTTGCT	360
ATAACCGTAT TATCTAAAAC AGCATAACAT TCAACATAGT GATCTCCTTT AAACGTGAA	420
TCTTCCGTGA TATTTTATTT TACCTGAAAA AATAGCACAC GCTCACAAATT CTTCTAATA	480
GCCTCAGCTT CAATATTCT TACTTTCCAA TAGACTCCCT GCGAAACAAA ATATGGTATA	540
GTAGTTCTAT GAATGATGAA GCAAGTAAAC AACTAACTGA TGCACGATTT AAGCGTCTTG	600
TTGGTGTTCAG CCGCACGACT TTTGAAGAGA TATTAGCTGT ATTAAAAACA GCTTATCAAC	660
TTAAACACGC AAAAGGTGGA CGAAAACCTA AATTAAGCCT AGAAGACCTT CTTATGGCCA	720
CTCTTCATA TGTGCGAGAA TATCGAACTT ATGAACAAAT TGCACGATTT TTTGGTATCC	780
ACGAAAGCAA CTTAATCCGT CGGAGCCAAT GGGTGAAGT AACTCTTGT CAAAGTGGTG	840
TTACGATTTA AAGAACTCCT CTCAGTTCTG AGGACACGGT AATGATTGAT GCGACGGAAG	900
TACAAATCAA TCGCCCTAAA AAAAGAATTA GCGAATCATT CTGGTAAAAA GAAATTCAC	960
GCTATGAAGG CTCAAGCGAT TGTACAAGT CAAGGGAGAA TTGTTCTTT GGATATCGCT	1020
GTGAACTATA GTCATGATAT GAAGTTGTTA AAAATGAGTT GCAGAAATAT CGGACAAAGCT	1080
GGAAAAATCT TGGCTGATAG TGGTTATCAA GGGCCCATGA AGATATATCC TCAAGCACAA	1140
ACTCCACGTA AATCCAGCAA ACTCAAGCCG CTAATAGCTG AAGATAAAGC TTATAACCCT	1200
GCGCTATCCA AGGAGAGAAG CAAGGTTGAG AACATCTTGT CCAAAGTAAA AACGTTAAA	1260
ATGTTTCAA CAACCTATCG AAATCATCGT AAACGCTTCG GATTACGAAT GAATTTGATT	1320
GCTGGCATTAG TCAATTATGA ACTAGGATTC TAGTTTGCA GGAAGTCTAT TATTTCCCTT	1380

ATTGTCTGTA AGTCTACTGA CCTTGGTTGTT TATCCCAGTC ATGGTTTCTA GTTCGGGCTC	1440
AGAGTTCAA AGTGGATGGC AAGAGCATCA ATTGATTGCT GAGAAGGTTA GTAAAACACT	1500
TGACAAGACA TTTGATAAGG ATGTCAGAAA AATTCCGACC AGTCCAGTTT TATCAAAAT	1560
TTGTAGATGA GATGGGAAGG ATTTACTC	1588

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 690 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTGTTTTAA TACAGCTAAC ATCTCTCAA AAGTGGTAGG CTGAACACCA ACAAGACGCT	60
TAAATCGTGC ATCAGTTAGT TGTTTACTTG CTTCATCATT CATAGAACTA CTATACCATA	120
TTTTGTTTCG CAGGGAGTCT AATATTGTCA AATACTGGAG CGCTCATTGC TGGTATACGG	180
AATAAGATTG GCCCAGCTTC GATAACTGGG ATACCTGGTT CAAAACCAAG ATCTGTTGCA	240
GCGATTGGTG TAAAGATATC GTAACCTTTC ATAAGGTCTT CGTTTACATC TTTCACCATG	300
ACTGCATCAC AGTGAACATC ATAACCACGG TTTGAAAGTT CTTCTCTAG AGCACTTTA	360
ATTGGTGAC TTGAGTTAAC ACCTGCACCG CAGGCAGCAA GAATTTAAAT CATTAGATT	420
TCCTCCGATT TTATTTTTA ATAGACAAGA TTAAGCGGTT GCTTCAGCAA TGTAAGCATA	480
AAGTTTTCT GGTCGGAAA TTTTGATAG GTCTTCAAGA TGTCCATTTC CTGTGAAAAA	540
GTCCATCAAC TGAGCCAGAA TATTTGTTG ACTTGAACCTT GAGTTATTGA TGATAAAGAA	600
GAGCAAGGAT ACTTCTACTT CCTTATCAGG AGCTATCATA TTGTGAAAAG TTACTGATT	660
TTCTAATCGA ACAACCACCA CTTTCTCAG	690

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ACTGCTACCT TTAAGAAGAT AGTAGACGTA TATACTTTT TAAGAAAATC AAAAAGATAC	60
TATAAAAAAT CTATTGTTT ATTGAATTAA AGACTTTGGT AACAAATTGA AAATAAAAAG	120

GAGGTATTCA TCATGAATAC AAAATGATG TCACAATTT CTGTTATGGA TAATGAAATG	180
CTTGCTTGC G TGAAAGGTGG AGATATTGAT TGGGAAGAG AAATTAGTTG TGCAGCAGGG	240
GTTGCATATG GCGCAATTGA TGGGTGTGCA ACAACGGTTT GATATTCTA TTGGGACCAT	300
TTGCTATAGG AATAGGTGTA ACTGGTGCTG CAGGTGGAG	339

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1693 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CTGAAGACCT CGTGCTACTC CTCCTCCAAC ACCTGCTTG GCAAATCTC CCCAATTGCA	60
TCCGCCACCT TCAACTCAAG CAAGCATCTC AGTATCCATA ATTTCAAATT GTGACATCTT	120
TTTTGTATTC ATAACGAATA CCTCTTTTT ATTNTTAATA TTTGTCTTGT TACAAACTTG	180
ACAAGTTTAG TATAACAGTA TCTATTAAATT TTTTCATCC AAATCTGAA TTGGCATCGA	240
AACGTCTTGA ATTAGCTTT TTGTTTCAAA ATCATCTCTA TTTTTAAAAAA AGATGTTTC	300
TAATCACTTT TTTACTATTT AGACTTCCTG CAAAATAGA ATCCTAGTTC ATGATTGATA	360
ATACCAAGCAA TCAAATTCA TCGTAATCCG AAGCGTTTAC GATGATTTCG ATAGGTTGTT	420
GAAAACATT TAAACGTTTT TACTTTGGCA AAGATATTCT CAACCTTGCT TCTCTCCTTA	480
GATAGCGCAT GATTACAGGC TTTATCTTCA ACTGTTAGCG GCTTGAGTTT GCTGGATTTA	540
CGTGGAAAGTT TGTGCTTGAG GATATATCTT CATGAGCCCT TGATAACCAC TGTCAGCCAA	600
GATTTTACCA GCTTGTCCGA TATTTCAT TTCTAAAAAC CATCTACTTC CGTTGACTTG	660
GAACCTCCGAT TGCTATTTTC CTTGAATGAT TTTAACCAAC TCTCCTACAC TTTGGAGTTG	720
GTCAATTTC TCATCGCTGA TTTCGATACT AAATTCACTCC TCCAGCGTCA AGATAAACTC	780
CATCAAATCA ACTGAGTCAG CATCCAAGTC GTCTTCAGA CTCAAGGATT CTGTCACGAC	840
AAAGTCTCT CCCTGTGCGT CTTGGATAAT GGTACAATAA CTGTAAAAAA TTTCTTTTC	900
TCTCATCTCT TTTATTCTCC TGAAAATTCA CGCGCAGTCT GGGCAACTAC TTCTGTTCT	960
AGCATGGTAC GAATCTGGCG AATCGTACTA TAAACAGCCCT TGGCATCGCT TGAGCCATGA	1020
GTCTTGACAA CAGGTGCCCT GACACCAAAAC AAGACCGCTC CACCAACATC TGAATAATTG	1080
AGCTGTTTTT TCAAACCTCT GAGGCTGTCC TTGAGAAGGA GGGCACCTAG TTTCGCTCGA	1140
AGACCACCAAC CTGTAATAGC TGTCTTGAGC AAGCCCCTGATGA TTCCCCTAGC TGTCCCTTCG	1200
ATGGATTGTA GCACAGCGTT TCCCCTGAAA CCATCTGCCA CAACAAACATC TGCAACGCCA	1260
TTCATCAAAT CACCGCTTC CACGTTCCG ATAAAGTTCA AACTTCATC AGCCGCCAGT	1320
AATTCTAAAG TTTCTCTACG AAGCGGGTCG CCCTTGCTAC TCTCTGTTCC GTTGTGAGC	1380
AAACCAACAC GTGGTTGC G AATGCCACGA ACATTCTTGG CATAGAAAGA ACCTAGGACA	1440
GCGTATTGAT GGAGGTGCTG GGCTGTATTT TCTGCATTAG CACCGAGGTC AAGCATGTCA	1500
AAACCTTCC CATCTACAGT CGGCAATGTT GACATAAGTC CAGGACGGTC GATATTCTTG	1560
ATACGACCCA CGATGAAGAA TCCAGCAGCC AACAAAGCAC CTGTATTCCC AGCCGAAAGG	1620

ACAGCGTCTG CTTCACCATC TTTGACAGCC TTGGCTGCCA ATACCATACT GGCATTTTC
 TTATTCCGAA TAG 1680
 1693

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 616 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTAAATCTGC TTGCTTAGTC CACTTGCTTG AGCCAAGGAG TCACATACTC AAAATTTCA	60
TGAAAGTCAT AGGTACCGTC TTCTTTTTA GCTGAAAAGA AAAGTCCATC GTGGTAGAGC	120
AAATCCCCGT GGGCCATAAT TCTGGCAGTT TTTTCCTCTT CCTACTCCTG AGACTTTGC	180
TTAGTCCCCCT CTTGAGAAAT AGTATCTCGT TTTTGACTAG TCAAGGGATT CCTTGGAAGC	240
TTTCAAACAA CAAGACCAAG CCCATTGATA AACCAACTGC TAGCAAGAGT ATGCCACAA	300
ATCCCTTATT GCTCCACTTG CGATAACTCC TAAAAAGTTT ACCAAGCCCT TCATAAAACG	360
AAAAGCTAAA CCACCCCTGAT TTCGATTTG TCTTCTTTGT ATCTTCGTTC TCCCTACTTT	420
CTTATGCAAG CCTTTCTTT TTATTATATC ACAGATAAGT ATTTCTTTCA CAATTGAATT	480
GAACCTCCCA TCTATTTCT ATAATCCTA AATGCCATAA TGCTTCAAT TCCTGTCATT	540
TTGTGATATC ATGTAGAAGA AATGAACCAA TCCACAGTGG CTTATTCCAA GTATACCACT	600
TGGGCTTTGG CAGTAG	616

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1973 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTAATATAGA ATAATCACCG CCGTTGTGAA AGAACGATTG GATGATAATC CAATCGTTCA	60
GGGAAATTGG AAGACCTTGG GTTCCAATT TAGGCATGAG ACACCTTGG TGGCTGCTGC	120
CGTCCCTCAC AAGCTAAGGT GATTGTTGAA AAAGAGGAAA AAGGAGAAGA AATGAAACCA	180
GTAATTCCA TCATCATGGG CTCAAAATCC GACTGGCAA CCATGAAAA AACAGCAGAA	240
GTCCTAGACC GCTTCGGTGT AGCCTACGAA AAGAAAGTTG TTTCCGCACA CCGTACACCA	300

GACCTCATGT TCAAACATGC AGAAGAAGCC CGTAGTCGTG GCATCAAGAT CATCATCGCA	360
GGTGCTGGTG GCGCAGCGCA TTTGCCAGGC ATGGTAGCTG CCAAAACAAC CCTTCCAGTC	420
ATTGGGTGTGC CAGTCAGTC TCGTGCTCTT AGTGGAGTGG ATTCACTCTA TTCTATCGTT	480
CAGATGCCGG GTGGGGTGCC TGTTGCGACC ATGGCTATCG GTGAACTCTT TTTTAGGATA	540
TAAAACAGGG TTCCGATAAG TTTTTTGCA AGGTGGATGA TGGCTACATT GTAATGTTTT	600
CCTTATTCTA ACTTAGTCTT AAGATAGGTC TAAAAACAG GTGAAAAGCG AAGGCATGCT	660
TTGGCAGCTT GTATGAGTAC CTACCGCAGA TGAAGGGAAC CCCGTTGAC CATCCTCCA	720
ACTAAATCAA TCTGACCTGA CTGATAAATA GAAGAATCCA GTCCAGCGAA AGCTTGTAA	780
TGAGCAGGAT TATCAAAGGC ATGAATATTT CGAATCTCGG CTAAAATGAC CGCCCCCTAAA	840
CGATTCTCAA TCCCAGTAAC CGTCGTGATG ACCGAGTTA ACTCAGCCAT CAAGTCATTG	900
ACACATTTT CCGCCCTGTC AATGAGCCTC TTGTAATGTT TGATGTTTC ATTACACGAG	960
ATAAAACGTC TATGCGTTAT CAAACTCATT ACCAATTAAA ACAAAATGTGG TTAGATCCTT	1020
TCGGAAATTG TCAAGCGATT GGAGGAAATG AACTAATCCA CAGCGGCTTA TTCCAAGTAT	1080
ACCACTGGG CTTTGGCAGT AGCTAATGTC GCTAAATATA ATATAAGGAG GAGTAAATG	1140
AAGACAGTTC AATTTTTTG GCATTATTTT AAGGTCTACA AGTTCTCATT TGTAGTTGTC	1200
ATCCTGATGA TTGTTCTGGC GACTTTGCC CAAGCCCTCT TTCCAGTCTA TTCTGGACAA	1260
GCGGTGACGC AGCTAGCCAA TTTAGTTCAA GCTTATCAA ATGGGCAATC CAGAACCTGT	1320
ATGGCAAAGC CTATCAGGAA TTCATGGTCA ATCTTGGCCT GCTGGTTTG GGTTCTATTT	1380
ATCTCTAGGT GTAATATAAA CATGTGTCTC ATGACGCGCG TGATTGCAGA ATCGACCAAC	1440
GAGATGCGCA AAGGTCTCTT TGGTAAGCTT GCTCAGTTGA CGGTTTCTTT CTTTGACCGT	1500
CGACAAGATG GCGATATCCT GTCTCATTAA ACCAGTGATT TGGATAATAT CCTCCAAGCC	1560
TTTAACGAAA GCTTGATTCA GGTGATGAGC AATATTGTT TATACATTGG TCTGATTCTT	1620
GTCATGTTT CGAGAAATGT GACGCTGGCT CTCATCACCA TTGCCAGCAC CCCATTGGCT	1680
TTCCATTATGC TGATTTCAT CGTAAAAATG GCACGTAAT ACACCAACCT CCAGCAGAAA	1740
GAGGTAGGGA AGCTCAACGC CTATATGGAT GAGAGCATCT CAGGCCAAAA AGCCGTGATT	1800
GTGCTAGGAA TTCAAGAGGA TATGATGGCA GGATTCTTG AACAAAATGA GCGCGTGC	1860
AAGGCAACCT TTAAAGGAAG AATGTTCTCA GGAATTCTTT TCCCTGTCAT GAATGGGATG	1920
AGCCTGATTA ATACAGCCAT CGTCATCTTT GCTGGTTCGG CTGTACTTT GAA	1973

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTAAACCAAT AGTTGCTGAA GACCATAATC CAGCTGCTGT TGTAAACCT TTAACCTTTT	60
GATTAGTTAC CATGATTGTT CCTGCCCTA GGAAACCCAA GCCACTAATT ACTTGGCTC	120
CCATTGACT AGGATCACCG CTACCATAAC GACTAGTGAT GAACTGATTGTCAT	180

CAACACAAGT TCCCAAACAA ACTAGTAAGT AGGTTCTAAT CCCTGCTGCT	TGGTTTTGA	240
CTCCTCGCTC ATAGCCAACA ATGCCACCGA AAAGAACATGC TAAAAAGCAC	CTAAGAAAGTA	300
TTTCCCAAAT ACTCAGTTCG TATGAAAGAT TCATATTATC TCTTACCTCG	TTTACCTTGG	360
AATAGGCTTG ATAAATAAAG AGCTGCACTA GACATAATCA TTAAAATTAC	AGAATAAACAA	420
AACATCATTG CCTGTGCATT TAAAGTTGCT GTTCATCAG TAGACTGTTT	AATAACGATT	480
CCCAATGGTT GGAAAAGTGG ATGGTACAAG AATACAGATA AGTCATAGTC	AGATAATAAA	540
GAATTAAAGT TTAACACAAAC TACTGATAAT ACGACTGGTA AAATATACGG	TATAATAACT	600
CGCACCATAG TGTAGAAACT AGATGCACCC ATACTACGTG CAGCTCTTC	CATATCATT	660
TCTATACTGA AAAATACAGC CGGAATCATT CTATAAGAAA ATGGTAATTT	TTGAATAGTA	720
TATGCAATAA GTAAAATAAT TACTGTTCT ACTAAAACTA AATTAAATAG	TATTAAATGA	780
GGTATATTAT AAGTGAACAT TAATCCTAGT GCAATCAATG TACCTGGCAA	TATCCATGGT	840
ATCAGTGCAC CATACTCAAA GAATTTATCG AACTTACTCT TGTTTTATG	TACAATACGT	900
GAAATTACTA TTGCTATAAT TGTAGCAATT ACCGCAGCTA AAATTGCATA	AACAACGCTG	960
ACTAGGTAAG GACGAAATGA TTGAGCATCT GTAAATAAT TAGCATAGTT	CGCTAACGTA	1020
AATTTAGATA GATCTAAAGT TCCCCTGTT ATCGTCAACG AGTCTGTAAA	CGAGTATAGA	1080
ATTATCAAAA CTATTGGAA CATATAGATT GCAAACAATA CATAAGCAGC	AATGTGAGCA	1140
AGAATTATTC CATAATGGAG AAGAAAATTA TCTGCTTCCT TAATACTAGC	CTGGTTTCG	1200
AAACAGAAAT		1209

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTAAGTCCTT TTAGTTTAT CTTAATTCTC TTATGTTGT AATAATCAAT	ATAGTCTATA	60
ATGGCTTGTGTT CCAATTGCTT AAGCGACTGA AACGACTTCT CATAACCGTA	AAACATTTCC	120
GATTTCAGAA TCCCAAAGAA AGATTCCATC ATACCGTTGT CTTGGCTGTT	TCCCTTGCCT	180
GACATAGATG CTTGAATTCC CTTACTCTTA GGAACCGATG ATAAGAATCG	TGTGGTATT	240
GCCAGCCTTG GTCACTATGG AGAACATGTAT TCTCGTAGTG CTTCTCTGTG	AATGCCCTGTT	300
CCAACATTGT TTGTACTTGT TCTAAGTTGG GTGAAGTTGA AAGATTATAG	GCGATAATTT	360
CGCTATTAAA GCCATCTAAA ACTGGTGATA AGTAAAGCTT TTGAGTACTT	GCTGGAATGG	420
CAAATTCTGT CACATCTGTG TAGCACTTT CCATTGTTT AGAGCCTTCA	AATTGGCCTT	480
GAATGAGATT CTCTGCCCTTC TTACCAACGT CTCCTTATG AGAAGATTTC	GTTTCTGTGCG	540
CATTTTAGCT TGTAAATTGA GTACTTTCAT CAAGCCTGAA ACTCTTTAT	GATTACCAG	600
ATAAGCACGA TTCCCTTAGTT CTAAATGAAT ACAGCGATAA GCATAATTTC	CCTTGTGTT	660
GATAAAAATG GATTGAATTT CAGCTTTAAG CTCTGGTCC TTATCTGGTT	TGTNTAG	717

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CTAAATCACC AGATTTAACCC AAGTCGTAGA TACGGCCTGG TGTTCCAATA ACAATATGAG	60
GCTGATTGCT TGCCAATTTC TCAATCTGGC GAGCCTTATC CGTACCAACCC ACATAATTAA	120
CCACACGAAC TTGCACATCT GAGTGAGCTG AAATCTGACG CGCTACTTGG TAAATTGAG	180
TAGCCAACTC ACGACTCGGT GCAGTAATCA CTGCTTGTAC ACTATCGCTA GCTTCATCTA	240
ATTGCTGGAA AATCGGTAAC AAGAAAGTAT GAGTCTTACC TGAAACCTGTT TTTGATTCTC	300
CTACTAGGTC ACGACCTGCC AAAACAATAG GAATCAACTT GTCTTGCACC TCTGTTGGAG	360
TTGTAAATT TAACTCCTCC AAGGCTTCTC TAATATAGTT TTTAAATTGA AATTTCGTAA	420
ATGACATAAC ATCCTCGATT CTATCTATCT TATCAATTAT ACCATATTAA ATTCCATTAC	480
AGTAGTCTCA CTTATTTAGG CTATTTCCAG TAGCTTCTCT AGTAAGAAAA GGCTGGAATT	540
TTATAGTTCC AACCTCTTT CAGTTATTAT TTCCAGTTA ACATAGCATT CAAGCCATAG	600
TGATCACTCA CTTGTGGACT CTTGTTACCA TCAAATACGA CATGAAATT TTCCACCGCT	660
AACTCTTGG TAGTAAAGAC ATAATCGATT CGAAGGGGTT CAGTGTCCC TTTCCAGCCA	720
TCAATTTCAG GCGGAACAGT ATAGCTACCA CTTTCTCTT GAGCAACTTC AAATGCGTCT	780
TGTAAGCCTA ATGGACTAGC TAAAATAGCT TGTTAACCTT CCCTGACCTG CTGGGTTGTT	840
AAAATCTCCA G	851

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTGTTGAGAT TGTTACGAAA TAACTGAAAA TATTTAAGGA GAAAATATAT GTTGAAACAC	60
TTAAACTTAA AAGGTCACTT ATTGACAGCC ATTCTCTATA TGATTCCAAT TGTTTGTGGT	120
GCAGGATTCT TAGTTGCCAT TGGTTTAGCA ATGGGGGGTG GTGTTCTGA CGCTCTTGTAA	180
GCAGGAAAAT TCACTATCTG GGATGCTTTA GCAACTATGG GTGGTAAAGC CCTTGGTCTC	240

TTGCCAGTTG TTATTGCTAC AGGTTGTCT TACTCGATTG CTGGTAAGCC AGGGATTGCA	300
CCAGGTTTG TTGTTGGTCT AATTGCCAAT TCTGTTGGTT CAGGGTTAT CGGTGGTATC	360
TTGGGAGGTT ATATAGTTGG TTTCTGGTT CAAGCGATTA TTAAAAAGGT CAAAGTACCA	420
AACTGGATTA AAGGTTTAAT GCCAACCTTG ATTATTCCCTT TTGTACCTCT TTGGTAAGTA	480
GTTTGATTAT GATTATATT ATTGGGGCGC CTATCGCAGC CTTTACCAAC TGTTGACGA	540
G	541

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTGGAATGAG TGTATAAGCC CAGCCAAGT TTTGCATCCG TTCAAAGTTC CAAGACCCTT	60
GTAAGAAGGT TGAACGCCAC CAAACTTTT TACGATCTGA TTTAGTTAAT TGAAGTTTT	120
CAGTCATGAT GTTTCAGTC CTTTCTTATC TTAGTAGTCT TCTAGGATAT CGCCGATTGG	180
GTCGTTAGAA GTTGGGGCTC CTCCGCCACC ATTCACCA GTTTAGAAA GGTGAAGGTA	240
GATAAGAGCG ATAGCAACAC CGATAGCACC GAATCCGATT AGAGTAATAT CTGACACAGC	300
AGCGAGAACG AAACCAAGAG CGAAGAATGG CCATACTTCA CGAGTTGCCA TCATGTTGAT	360
AACCATGGCG TAACCAACGG CAACGACCAT ACCACCACCG ATAGCCATAC CATCTTGAG	420
CCAGTCTGGC ATGGCACTAA GGATACTTG TACAGTTCA GTTGGTACCA TAAGGAGAAG	480
AGCTGCAGGA AGCGCGATAC GAAGTCCTTG GAAAAGTAGC GCAATGAAAT GCGCACGCTC	540
CACAGCGCCG AAGTCACCTT TTTTAGGGC AGCATCTGCA GTATGAACCA AACCAACTGA	600
AATTGTACGA ACAATCATTG TCAAGAAAAG TCCAGCTACG GCAAGAGGGA TAGCAACCGC	660
TTGGGCAACA CCGATACCAAG TCTTGGTAAA GTCACCACCA AGAACCATGA TAATGGCAGC	720
AGCGACAGAA GCAAGTGCAG CATCAGGAGC GATAGCAGCA CCGATATTG ACCAACCAAG	780
GGCAATCATT TGAAGCGATC CACCGAGGAT AATCCCTGCT TCCAAGTGGAA CCTGTTACAA	840
GCCCATAAG GGTACAGGCT ACAAGTGGTT GGTGAAATTG GAACTGGTCG AGGATGCCTT	900
CAAGACCTGC AAAGGAAGGC TACAACGACT ACTAAAACCA TAGAAATAAT AGACATGTTT	960
AAAATCCTT CATAAATAAT GGCTTATTG ACATTGGCTT TGTTAATCAA GTCAAACAAA	1020
TCTTTTTAG AATCATTG TACTTACGG ACATCAAATT CAACACCCAA GTCACGCATT	1080
TTTTCAAATG TAGCAACATC TTCTTGTCC ATAGACAAAA CGGTATTGAC CAATGTTTA	1140
CCTGTTGAGT GAGCCATAGA ACCAACGTTA AGAGTCTTGA TTGGCACGCC GCCTTCGATG	1200
GCACGAAGGG CATCTTGAGG TGTTTCAAAC AAGATAAGGG CATGTGTTTC TCCAAAACGT	1260
GGGTCTTTG AAATATCAAT CAGTTTTGA ATTGGAACCA CGTTAGCCTT GACATTACCT	1320
GGAG	1324

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TCATAAGGAA	GCTGTCGCTC	GTTCCGCTAA	GGTATGGACA	CCACGGTGAA	CATTGGCATT	60
GTCCCTGCTCA	TAGTAACTGT	TAATAGCTTT	CAGAACTACT	AGTGGTTTTT	GTGTCGTCGC	120
AGCATTGTC	AGATAGACCA	GAGGTTCATC	ATTGACAATC	TGATCTAAAA	TTGGAAAATC	180
CTTGCGAATC	GCTTCTACAT	CTAACATAGG	CTTCCCCTTA	GCCTTTGAC	AATTCTCTTT	240
CGATAGTTGC	AATCATTCA	TCACGAACCT	CCTTGACTGG	AATCTCCACG	ATAACAGATC	300
CAAGGAAACC	ACGAACAAACC	AAACGCTCTG	CAGTTGCCCT	ATCCAATCCA	CGACTCATGA	360
GGTAATACAT	GTCTTCTGGA	TCAACTTGTC	CGATAGACGC	TGCGTGTCCCT	GCAGTGACAT	420
CATTTTCATC	AATCAAAAGA	ATTGGGTTAG	CATCTGAACG	CGCTTGGTCT	GAAAGCATGA	480
GAACACGGCT	CTCTTGTGTC	GCATCTGCTC	CCTTAGCACC	CTTGATGATG	TGGCCGATAC	540
CATTGAAAGT	CAAAGTTGCT	TTTCAAGGA	TAACCCCATG	TTGTAGGATA	TTTCCGATAG	600
AGTTGCAGCC	ATAGTTAGTT	ACACGAGTAT	CAATCCCTTG	TACCTGACGA	CCACTTGAAA	660
GAG						663

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 649 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CTAGTTGGAT	GGCTTCAATA	AAGGATGATT	TGGCTGCTCC	ACTATTGGCA	ATGAGCTGAA	60
AACAGATATA	TTCCATTCT	TCGTCATCTT	ATTTCTCCTA	TCCATTCAAG	TGCTTGTTC	120
AGAACTTTG	CTCCATTCA	CATTCCGTA	TCCCGCATAT	CAATGGTATC	TACAGGGATA	180
TTTCCTGCAA	TTTCTTCAC	AGCAAGTAAC	TCATAACGAA	TTTGTGGCCC	AATTAGAATG	240
ACATCTGCTT	CATGGATATT	CTTTTTAGCT	TCTGTCATTG	ATTTTGCTTG	GATAGAAATT	300
TCAATCCCAC	GTTCAGTCGC	ACTTTGTTGC	ATTTTTTAA	CAAGCATACT	TGTCGACATT	360
CCCGCATTAC	ATACTAATAA	AATTGTTTC	ATAATCTAA	CCTTCATTT	CTTGTCAAC	420
AACTTTGTCA	TTAACCTTGA	TAAATGGAAT	GTATAGAAGA	ACTCCAAGTG	CAAAGATGAT	480

GAATTGAACT AGAACTGCTC TCACGTCCCC TGCTGTTGCT AACCATGCAT TTAAGAATA	540
TGGTAGTC CAAGGAACCT GTATAAATGC AGGACTCATG AATCCTGTAA CTGTTGCTAA	600
GTAGCTGATT AAAATACCAA GGACTGGAAC TGTGATAAAT GGAATAGTC	649

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CTTGGTATTA TTTGAAATCA GATGGTTCTT ATGAAAAAAA TGCATGGCAA GGAGCTTATT	60
ACCTTAAATC AAACGGTAAA ATGGTACAAG GTGAGTGGGT TTATGATTCT TCTTACCAAG	120
CCATGGTATT ACTTGAAATC AGATGGTCA TATGCTCGCA ATGCATGGCA AGGAAACTAC	180
TATTTGAAAT CAGATGGTAA AATGGCTGTC AATGAATGGG TTTATGATGC CACCTATCAA	240
GCATGGTATT ATTTGACATC AGATGGTTCT TATGCTTACA GTACATGGCA AGGAAATTAC	300
TATCCTAAAA TCGGATGGTA AAATGGCTGT CAATGAATGG GTTGATGGTG GACGTTATTA	360
TGTTGGCGCT GACGGAGTTT GGAAGGAAGG TCAAGCAAGT ACAGCTTCTC CTAGTAATGA	420
TAGCAATAGT GAATATTCT GCTGCTTTAG GAAAGGCAAA AAGTTATAAT TCGTTATTCC	480
ACATGTCAAA AAAAACG	497

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTAGTCTAAA TTTTTAAAAA CAAAGGTCAA AGATAGTCAT TATCAGTAAT CATAACTAAG	60
TAAACAAAAA GAGGTAAAGA ATATGAATAA CAACTTTAAT AATTTTAATA ACATGGATGA	120
TTTATTTAAC CAATTGATGG GTGGTATGCG AGGATAACAGT TCTGAAAATC GCCGTTACTT	180
AATTAATGGA CGCGAAGTCA CACCTGAGGA ATTGCTCAC TATCGTACGA CTGGTCAATT	240
ACCAGGAAAT GCAGAAACTG ATGTGCAAAT GCCACAAACAG GCATCAGGTA TGAAACAAGA	300
CGGTGTCCTT GCAAAACTAG GTCGAAACTT GACAGCAGAA GCGCGTGAGG GCAAGTTGGA	360

TCCTGTTATC GGACGAAACA AGGAAATTCA AGAACATCT GAAATCCTCT CACGCCGCAC	420
CAAGAACAAAT CCTGTTTGG TCGGAGATGC AGGTGTTGGT AAGACAGCAG TTGTCGAAGG	480
TCTAGCGCAA GCCATTGTGA ACGGAGATGT TCCTGCTGCT ATCAAGAACAA AGGAAATTAT	540
TTCTATTGAT ATCTCAGGTC TTGAGGCTGG TACTCAATAAC CGTGGTAGCT TTGAAGAAAAA	600
TGTCCAAAAC TTAGTCAATG AAGTGAAGA AGCAGGGAAT ATTATCCTCT TCTTTGATGA	660
AATTCAACCAAA ATTCTTGGTG CTGGTAGCAC TTGTGGAGAC AGTGGTTCTA AAGGGCTTGC	720
GGATATTCTC AGCCAATCGA TCTCTCTCGT GGAGAATTGA CAGTGATTGG GGCAACAACT	780
CAAGACGAAT ACCGTAACAC CATCTGAAG AATGCTGCTC TTGCTCGTCG TTTCAACGAA	840
GTGAAGGTCA ATGCTCCTTC AGCAGAGAAT ACTTTTAAAAA TTCTTCAAGG CATTGGTAC	900
CTCTATCAAC AACACCACAA TGTCATCTTG CCAGACGAAG TCTTGAAGC AGCGGTGGAT	960
TATTCTGTTCA AATACATTCC TCAACGTAGC TTGCCAGATA AGGCTATTGA CCTTGTGAT	1020
GTAACGGCTG CTCACTTGGC GGCTCAACAT CCAGTAACAG ATGTGCATGC TGTTGAACGA	1080
GAAATCGAAA CGGAAAAAGA CAAGCAAGAA AAAGCAGTTG AAGCAGAAGA TTTTGAAGCA	1140
GCTCTAACT ATAAAACACG CATTGCAGAA TTGGAAAGGA AAATCGAAAAA CCACACAGAA	1200
GATATGAAAG TGACTGCAAG TGTCAACGAT GTGGCTGAAT CTGTGGAACG AATGACAGGT	1260
ATCCCAGTAT CGCAAATGGG AG	1282

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CTTGATATAA TTCTTGTTC GAAAGATTCT CCTTAGGTAT ATCTATTCTT CCACTAGTAA	60
ACGGTAATTC CAAAACAGAG TTTACTTCGT TAAATGTAAG CCAATATTAA ACTTTATCTT	120
TATACCTTTC TAAAACGTGTT CGAGCAAATT TTTCATAAAA ATGAATCATT CTTCCATATCA	180
ATCCCATCCAT GATATTTCT TGCTAAATAT AATGGAGTCT CATACTGTGA AAGAGTTACA	240
AGTGGTTCTA TCCCCTGAGC ATGTAGTTCA TCAAACAATT CATCATAATA TTTCAATCCA	300
GCTTCGTAG GTTCTTCCTC ATCTCCTTTT GGAAAAATTTC TACTCCATGC AATAGAAGTA	360
CGAAAAACAT TAAAGCCAT TTCAGAAAAC AAGGATATAT CTTCCCTATA TTTATGATAA	420
AAATCAATAC CTATCAATT TAAAGTTATCT TCTGTAGGAT TTTCTGTTGC TTCTCCTAAT	480
CCACCTTTGG GTAACACATC CTGAACGTAT AACCCCTTAC CATCTTCATT ATATGCTCCC	540
TCTACTTGAT TAGCTGCAAC AGCTCCACCC CAAAGAAAAT CATCTGGAAA AATGGTCATA	600
ACTTTCCCTCC ATTATAATAT TACCACTAAT TCCTTAGAAA TGCTCGATTG TCTGATTATT	660
AGGTAATATT AATACATCTA GAAAATCATT GGTATTGTT ACAATTACTG GTGTAACGT	720
TTCGTAGCCT TTAGTCTTGA TTAAATTCAA GTCCATTCA AAAATCAACT GATTTTGAA	780
AACTCTGTCT CCTTCTTCTA CATGACTAAT AAAACCTTGA CCTTTAG	828

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AGCTATGGTC AGACTCAGAT TGATGGCGTT GCTTATGCCA AGTACGATAT CTTCCGTTTA	60
AAGAACGGGA AAATTGTGGA GCATTGGGAT AATAAGGAAG TCATGCCTAA GGTAGAAAGAC	120
TTGACCAATC GAGGGAAAGTT TTAAATTGAG GACAAAGAAAT GATTGAATAC AAAAATGTAG	180
CACTGCGCTA CACAGAAAAG GATGTCTTGA GAGATGTCAA CTTACAGATT GAGGATGGGG	240
AATTATGGT TTTAGTAGGG CCTTCTGGGT CAGGTAAGAC GACCAGCTC AAGATGATTA	300
ACCGTCTTT GGAACCAACT GATGGAAATA TTTATATGGA TGGGAAGCGC ATCAAAGACT	360
ATGATGAGCG TGAACCTCGT CTTTCTACTG GTTATGTTT ACAGGCTATT GCTCTTTTC	420
CAAATCTAAC AGTTGCGGAA AATATTGCTC TCATTCTGA AATGAAGGGG TGGAGCAAGG	480
AAGAAATTAC GAAGAAAACA GAAGAACTTT TGGCTAAGGT TGGTTTACCA GTAGCCGAGT	540
ATGGGCATCG CTTACCTAGT GAATTATCTG GTGGAGAACCA GCAACGGGTC GGTATTGTCC	600
GAGCTATGAT TGGTCAGCCC AAGATTTCC TCATGGATGA ACCCTTTCG GCCTTGGATG	660
CTATTCGAG AAAACAGTTG CAGGTTCTGA CAAAAGAATT GCATAAAGAG TTTGGGATGA	720
CAACGATTTC TGTAACCCAT GATACGGATG AAGCCTTGAA GTTGGCGGAC CGTATTGCTG	780
TCTTGCAGGA TGGAGAAATT CGCCAGGTAG CGAATCCCGA GACAATTAA AAAGTGCCTG	840
CAACAGACTT TGTAGCAGAC TTGTTGGAG GTAGTGTTC A TGACTAATT AATTGCAACT	900
TTTCAGGATC GTTTAGTGA TTGGTTGACA GCTACAATGA CATTGGTCGG TTCCTTGAGC	960
AAGAGATAGA TTAGCCAGAC AGTCATGCCA AAAATCCCTC CAGGTAAGAG CATAGACCGT	1020
TGCACATTA GTACGATTAA AAAAGTGATA ATGGCAAGAA AACTTGCTAC TGCTTGTAAT	1080
AAAAAGGTTG TTAGTGTCA ATTAGTCAT CAATACCAAG GCGACAGAAC TTCCCTGCC	1140
TAAAGCGAGG GTAATGAGCA GGGATTCAAA CATCTTACTC ATACCAAGAGT TTATGTGGTT	1200
GGTCATAATA TCACGGACCG CATTGGTCAA GGCAATACCT GGTACAAACG GCATGACCCG	1260
ACCAGCTATA ATCAAATCCT GCCCGTTGA ATGGAAAAC CCTGTGTTAG CCGAGCCCCA	1320
AAACTGGGGC CAATTATCC CCCAAAGACA AAAGCTCCAT CAAAGGCTGT CACAAAGGGA	1380
ATTGGATAA ATTTCCACA TAGAAGGAAA AGGCAAAACC AAATAAGGTC GCCACTCCTG	1440
CCCCAAGTGC TCGTAAATAT TCCGCT	1466

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AAGGTTCTTC GTAAATGTAC ACCATTGGAA TGCTAAAAAT GGTTCTGAA GCTGCTGCTA	60
AATCTGCACA AGAACACGGT CTTAAATCAG TTGAAGTTAC TGTAAAAGGT CCAGGTTCTG	120
GTCGTGAGTC AGCTATTTCG TGCGCTTGCT GCCGCTGGTC TTGAAGTAAC AGCAATTCTG	180
GATGGGACTC CAGTGCCAAC ACAATGGTGC TTCGTCCCTCC AAAACGTCGC CGTGTATAAT	240
CATCGCATT AACTGCTTTT CGTTAAGAG CGAGTAAC TAATGATCGAG TTTGAAAAAC	300
CAAATATAAC AAAAATTGAT GAAAATAAAG ATTATGGCAA GTTAGTAATC GAACCACCTG	360
AACGTGGCTA CGGTACAGCT CTTGGTAACT CTCTTCGTG TGTAATTCTA GCTTCTCTAC	420
CAGGAGCAGC TGTGACATCT ATCAACATTG ATGGTGTGTT ACATGAGTTT GACACAGTTC	480
CAGGTGTTCG TGAAGACGTG ATGCAAATCA TTCTGAACAT TAAAGGAATT GCAGTGAAT	540
CGTACGTTGA AGACGAAAAA ATCATCGAAC TGGATGTTGA AGGTCTGCT GAAGTAACAG	600
CTGGTGACAT TTTGACAGAT AGCGATATTG AAATTGTAAC TCCAGATCAT TATCTCTTA	660
CAATTGGTGA AGGTTCTCT CTAAAAGCGA CTATGACTGT TAACAGTGGT CGTGGATATG	720
TACCTGCTGA TGAAAATAAA AAGGATAATG CACCAGTTGG AACACTTGCT GTAGATTCTA	780
TTTATACACC AGTTACAAAAA GTCAACTATC AAGTGGAACC TGCTCGTGA GGTAGCAATG	840
ATGGTTTCGA CAAATTAAACC CTTGAAATCT TGACAAATGG AACATTATT CCAGAAGATG	900
CTTTAGGGCT TTCAGCACGT ATTTTGACAG AACATCTTGA TTTGTTTACA AATCTTACTG	960
AGATTGCTAA GTCAACTGAA GTGATGAAAG AAGCTGATAAC TGAATCTGAC GACCGTATTT	1020
TAGATCGTAC GATTGAGGAA CTGGACTTGT CTGTGCGTTC ATACAACGTG TTAAAACGTG	1080
CCGGTATCAA TACTGTGCAT GATTGACAG AAAAATCTGA AGCAGAGATG ATGAAAGTAC	1140
GAAATCTTGG ACGCAAGAGT TTGGAAGAAG TGAAACTCAA ACTCATTTGAT TTGGGTCTTG	1200
GATTAAAAGA TAAATAAAGG AGGAATACAT GGCTTACCGT AAACTAGGAC GCACTAG	1257

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTATTGAAAC AAGAAAAATA GAGAATCAA GAAAGAGAAC TTATGAATAT TCAAGAAGAA	60
ATTAAGAAC GTCGTACCTT TGCCATTATC TCCCACCCGG ACGCGGGGAA AACAAACCATC	120
ACTGAGCAGT TACTCTAACT TTGGGGGTGA GATTGCGAG GCTGGTACGG TAAAAGGGAA	180
GAAAACAGGG ACTTTGCTA AATCTGACTG GATGGATATC GAGAAGCAAC GTGGGATTTC	240

TGTTACTTCA	TCTGTTATGC	AATTTGACTA	CGACGGCAAG	CGCGTGAATA	TCTTAGACAC	300
GCCAGGGCAC	GAGGACTTCT	CAGAAGATAC	CTATCGTACC	TTGATGGCGG	TGGATGCTGC	360
GGTCATGGTC	GTGGACTCTG	CCAAGGGAT	CGAGGCTCAA	ACAAAGAAAT	TGTTTGAGGT	420
TGTGAAACAT	CGTGGCATT	CAGTCTTAC	CTTATGAAC	AAGTTGGATC	GTGACGGTCG	480
TGAGCCTTG	GATCTTGC	AAGAATTGGA	AGAAATCTT	GGCATTGCTA	GCTACCCCTAT	540
GAAC TGGCCT	ATCGGGATGG	GGAAAGCCTT	TGAGGGCTTG	TATGACCTCT	ATAACCAACG	600
TTTAGAGCTT	TACAAAGGGG	ATGAGCGTTT	TGCTAGCCCT	AGAAGATGGA	GACAAAAC	660
TTGGTAGCAA	TCCTTCTAC	GAGCAAGTCA	AGGATGACAT	TGAGCTTTA	AATGAAGCTG	720
GGAATGAGTT	TTCAGAGGAA	GCTATTCTGG	CTGGAGAATT	GACGCCTGTC	TTTTTCGTT	780
CAGCCCTGAC	AAACCTTGCT	GTGCAGACCT	TCCTTGAAAT	CTTCCTCAAG	TTTGCTCCAG	840
AACCACATGG	TCACAAGAAA	ACAGACGGTG	AAATTGTGGA	TCCTTATGAC	AAGGATTCT	900
CAGGCTTTGT	CTTTAAAATC	CAAGCCAACA	TGGATCCTCG	TCACCGTGAC	CGTATTGCT	960
TTGTCCTGAT	CGTATCAGGC	GAATTGAGC	GTGGCATGAG	TGTCAATCTC	CCTCGTACTG	1020
GTAAGGGTGC	CAAACATATCT	AATGTTACCC	AGTTTATGGC	GGAGAGTCGT	GAGAATGTGA	1080
CCAATGCCGT	AGCAGGTGAT	ATTATCGGGG	TTTACGATAC	CGGTACTTAT	CAGGTTGGGG	1140
ATACCTTGAC	GGTTGGAAAA	AAACAAGTTG	AATTGAAACC	ACTGCCAAC	TTTACTCCTG	1200
AAATTTTCAT	GAAAGTTTCT	GCTAAGAATG	TTATGAAGCA	AAAATCCTTC	CACAAGGGGA	1260
TTGAGCAATT	GGTGCAGGAA	GGAGCCGTT	AGCTTATAA	GAATTACCAA	ACAGGTGAGT	1320
ACATGCTGGG	AG					1332

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 932 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TTGGACGCTG	GAACAAATCC	AAGCTGACCT	GTTCCAAGAC	CAGACTTGGT	ATGCTCTGGC	60
TTATGATGGG	GCAGAAAGTGA	TTGGCTTCT	AGCTGTTCA	GAGACTCTTC	TTTGAAGCAG	120
AAGTCCTGCA	AATCGCTGTC	AAAGGAGCCT	ATCAGGGTAA	GGGCATTGCG	TCAGCCTTGT	180
TTGCTCAATT	GCCGACAGAC	AAGGAAATTT	TCCTCGAAGT	CAGACAGTCA	AATCAACGAG	240
CGCAAGCATT	TTACAAGAAA	GAAAAGATGG	CAGTTATCGC	TGAGCGAAAG	GCCTACTACC	300
ATGACCCAGT	CGAGGACGCC	ATTATCATGA	AGAGAGAAAT	AGATGAAGGA	TAGATATATT	360
TTAGCATTG	AGACATCCTG	TGATGAGACC	AGTGTGCGCG	TCTTGAAAAAA	CGACGATGAG	420
CTCTTGTCCA	ATGTCATTGC	TAGTCAAATT	GAGAGTCACA	AACGTTTTGG	TGGCGTAGTG	480
CCCGAAGTAG	CCAGTCGTCA	CCATGTGAG	GTCATTACAG	CCTGTATCGA	GGAGGCATTG	540
GCAGAAGCAG	GGATTACCGA	AGAGGACGTG	ACAGCTGTTG	CGGTTACCTA	CGGACCAGGC	600
TTGGTCGGAG	CCTTGCTAGT	TGGTTGTCA	GCCGCCAAGG	CCTTGCTTG	GGCTCACCGA	660
CTTCCACTGA	TTCCTGTTAA	TCACATGGCT	GGGCACCTCA	TGGCAGCTCA	GAGTGTGGAG	720

CCTTTGGAGT TTCCCTTGCT AGCCCTTTA GTCAGTGGTG GGCACACAGA GTTGGTCTAT	780
GTTTCTGAGG CTGGCGATTA CAAGATTGTT GGAGAGACAC GAGACGATGC AGTTGGGGAG	840
GCTTATGACA AGGTGGTCA TGTCATGGGC TTGACCTATC CTGCAGGTCG TGAGATTGAC	900
GAGCTGGCTC NTCTNGGGCA GGANATTAT GA	932

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1158 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTAAACTTTC GCTCATAGGC ATACAAATTA ATCCTTGCG ATAAGTAGCC ATAAAATTAA	60
CATTTTCTGT TGTAGCTGCT TGTGCGAAC AAATTAAGTC TCCTTCATTT TCTCTATCCT	120
TGTCGTCTAT AACAAAGAAC AAGTCGTCCT TCTGCAATGC TTCTAATGCT TCTTGTATTT	180
TTCGATATTC CATTGACTGA TTATCCTTTC TGCTAAAATC CATTGGATA TAATAGTTCC	240
TTCGATATTT CTGATTTGG AGAGTTATCC ATCAGTTTT GCACATATTT ACCTAAGATA	300
TCATTTCAA GATTTACTGT ACTCCCCACT TGTTTACTCT TAAGAATGGT TTGTTCAAG	360
GTATGAGGGA TAACAGATAC TGAAAAGTTT ACTTTGGAGA CTTTAGCGAC AGTCAGACTA	420
ATGCCGTCAA TTGTAATAGA TCCTTTTCA ACTATTAAAT CTAAAATTTC TTTTTGTGTG	480
TTGATTTGAT ACCATACAGC ATTATCATCT TTTTTTATIG ACGAGATTT TCCTGTACCA	540
TCAATGTGTC CTGTAACGAC GTGACCCCCA AGTCGACCGT TGACAGATAA GGCTCTTCT	600
AGATTCACCT CACTTCCATG TTTTAATAGA GTAAGAGCTG TTCGACTCCA TGTTTCATTC	660
ATTACATCAA CTGTAAAGGA TTGATGATTG AAATGAGTAA CTGTAAGACA GATACCATT	720
ACTGCTATAC TATCGCTAA ATGGATATCC GTTAATATTT TTGAGGCTTT AATTGATAGT	780
TTACAATTAC GAGAGTCTTT CTGTATTCCT TCAACTTTTC CGATTTCTTC AATTATTCC	840
GTGAACATGG ATAAATCACT TCACTTTCTA TGAGATAGTC NTTCCCTNTT TGAGAAAAAG	900
CATAAGGTTT CAATCTAATA GCGTCATTTG GCAAAGAAAT GCCTTCACCT CCGACAGGAA	960
ACTTGGCACT GCCTCCAAAA ATTTTGGTG CAATATATAT TTTCAGCTCA TCAACAAATT	1020
GTGTTCCAA AGCACTCCAA TTCATTAGAC TGCCCCCCTC TACAACTAGG CTATCAATCT	1080
GCATGTTCC TTAGATGTTN GCATTAAGTC TATATGATTG CCTTTTTCT	1140
TTATGGAAAG TATTCCCC	1158

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TAAAGGCTGT TTGGATAATG TAACATAAAG AAATCTTGTG	60
TCCTGAAGTG ATGACTTCTT TATTAGACAT AATGTCTGGA CCCAAGATTAA	120
AAAGAACCGCC CGCAAGAAT ACGAGCATCA AAGGTAGCAG ATGCAACAAAC	180
TGTATCGTGG AAGATTGAGA GGAACCTTAGG TAATTTAAGA TTGTCTAAAC	240
TTTCTTCTTT CTTACCAAAG CGTCCTGCTA CTTTATCTAC AAACCAGATT	300
GCAAATTGCT GTTGGTGACC AATCGCAAAT CCGCCACCAC CAGTCAAGCG	360
TTGAGTTGCC TCAACAGTCA TATTGAACT AACTGCCAG TAAAGTCCAC AGATGATACC	420
AATCGCTGCT GTACCGTAAG CATTCGCAA TTGTGGTACT AAGAATAGAA CCATAAGAGA	480
TACTGTTGCA GCTAGCCATG CTGATCAATT CCCTCAACCA GTCCTATATC TCAGCCAAGA	540
GAATCGAGGA GGTCTTGC GAATCTCCCG AAAACATCCA TTCAGAATTAA	600
GAACAAAAGC AAGTTACCAAG TGTCGGGTT TTACAAGTCC AAGAATTGAC	660
TTTTACCTAT CCTGATGCGG CCCAGCCTTC TCTGAGAGAC ATTTCCTTG ATATGACTCA AGGACAAATC	720
CTTGGTATCA TTGGGGGGAC TGTTCTGGT AAATCAAGCT TGTTGCAAAT CTTACTTGGA	780
CTTTATCCAG TAGACAAGGG GAACATTGAC CTTTATCAAA ATGGACGTAG	840
TCCTCTTAAT TTGGAGCAGT GGCGGTCTTG GATTGCCTAT GTACCTCAAA AGGTCAAATC	900
CTTAAAGGGA ACTATTGTT CCAACTTGAC TTTAGGTTA AATCAAGAAG TATCTGACCA GAAACTCTGG	960
CAGGCCTTGG AGATTGCGCA AGCTAAGGAT TTTGTCAGTG AAAAGGAAGG ACTTTTGGAT	1020
GCCCTAATTG AAGCAGGGGG GCGAAATTG TCAGGTGGAC AAAACAAAG GTTGTCTATC	1080
GCCCCGAGCAG TCTTGCCTCA AGCTCCGTTT ATCATTCTAG ATGATGCAAC CTCGGCACTG	1140
GATACCATTAA CAGAGTCCAA GCTCTTGAAA GCTATTAGAG AAAATTTC	1200
AAACACGAGC TTAATTGAA TCTCTCAACG AACCTCAACT TTACAGATGG CGGACCAAGAT	1260
TCTCCTCTTG GAAAAAGGTG AGTTGCTAGC TGTTGGCAAG CACGATGACT	1320
TGATGAAATC CAGCCAAGTC TATCGTAAA TCAATGCATC CCAACATGGA AAGGAGGACT	1380
AGAATGAAAC GACAAACTGT AAACCCAGACG CTCAAACGTT TAGCCGTAGA	1440
TTTAGCAAAC CATCCCTTCC TCCTTTTCCT AGCCTTTCTA GGAACATATTG CCCAAGTTGG	1482
CTTATCAATT TACCTACCTA TTCTGATTGG GCAGGTCATT GACCAAGTCC TAGTGGCTGG	
TTCATCACCA GT	

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 895 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CTCTGAAGGA TCCAGAAAAT CGCTTATATA TTTTATTAAA AGACGGTCAG GTTATTGGGA	60
CTTGTACGGT TGATTTATCG ACTAATACGA ATTACTCTA CGGTTTAGCA ATATTGAAAC	120
CTGAACGTGG AAAAGGCTAT GGAAGCTACT TAGCAAATC CCTCGTCAAC CAACTAATTG	180
AGCAAAATGA CAAGGAATT CAGATTGCAG TGGAAGATAG CAATGTAGGT GCCAAACGTT	240
TGTATGAAAA AATTGGCTT GTCAAACAGA CTCAGGTGGT TTATCTGAAT GAGAAAGGAG	300
CAAGGGATTC CGAAGTGTAG AGATATTCGG ACTGAAATT ACTTGAACCTT TTAGTGATGA	360
AACTAATTGT TCTTGGATT CAGCTTCCT GATTATGATT TATGATTAAA ATCTATGACA	420
CCATGTCTCG TGATTTGCAGA GAATTGTCC CGATTGAGGA CGGCAAGATC AAGATGTATG	480
TTTGTGGGCC AACGGTGTAC AACTATATCC ACGTGGAAA CGCCCGTTCG ACGGTAGCTT	540
TTTTGGATAC GAATTTCGTC GCTATTGTA GTACCGTGGG TATAAGGTTG CCTATATTTC	600
CAATTTACA GATGTGGATG ATAAGATTAT CAACCGTGCC AGGGAAGAAG GCATCACGCC	660
TCAGGAGGTT GCGGATAAGT ACATCGCTGC CTTTCGTGAG GATGTGACGG CCTTGGCGT	720
GAAACCTGCG ACTCGCCATC CGCGTGTAGT GGAGTTTATG GCAGACATCA TCCGTTTGT	780
GGAAGACTTG ATCGAGAAAG GCTTTGCCTA TGAGAGTCAA GGGGATGTCT ATTTCCGTGT	840
AGAAAAATCC CACAACATATG CTAAATTGGC TAATAAAACC TTGGAAGATT TGGAG	895

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 709 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTGTTTGCCTTCTAA TAAAGAATTG GCAGAACGTG TGGCGCAGGA GATTGGGATA	60
GAGTTGGGAA AATCAAGTGT TCGCCAATTTC TCAGATGGAG AGATTCAGGT CAACATTGAA	120
GAATCAATCC GTGGGAAACA CGTCTTTATC CTACAATCAA CTAGTTCGCC TGTAAATGAC	180
AATCTGCTTG AAATTTGAT TATGGTAGAT GCTTTGAAGC GTGCGAGTGC AGAATCTGTC	240
AATGTTGTCA TGCCTTACTA TGGGTATGCA CGTCAGGATA GAAAGGCGAG AGCGCGTGAG	300
CCAATCACTT CAAAACCTGT CGCAAATATG CTTGAAGTAG CTGGAGTGGA TCCTTATTG	360
ACCATCGACT TGCATGCTGC GCAAATTCAA GGATTCTTTG ATATTCTGT GGATCATTTG	420
ATGGGTGCTC CTCTGATTGC AGATTATTTT GAGCGTCCTG GTATGGTTGG TTCTGACTAT	480
GTGGTTGTCA GCCCGGACCA TGGAGGGGTG ACTCGTGCTC GTAAGTTGGC AGAATTTTG	540
AAAACATCTA TCGCTATTAT TGAGAAACGT CGTAGCGTTG ATAAGATGAA TACTAGTGA	600
GTTATGAACA CCATCGGTAA GGTTGAAGGC AACCACTTGT AGCTTCGATT GATGATATGT	660
ATTGATACCG CTGGAACGAT TTGTCATGCG GCAGATGCTC TTGCGGAAG	709

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CTAGAAGAAC TCCGTCACAA GCTTGTGACT TGTAAGCAAG AACAGAGCAA GATTGAGGAT	60
TCCTTATGAT TTCATTCCTT CTTCTATTGG TCTTGGTTTG GGGATTTTAT ATCGGCTATC	120
GGAGAGGCCT GCTCTTACAG GTTTATTACC TGATTTCAGC CATGGCATCG GCTTTTATGG	180
CTGGCCAGTT TTATAAGGGG CTTGGAGAGC AATTCCATTT ATTGCTCCCT TATGCAAATT	240
CGCAGGAAGG TCAGGGGACT TTCTTTTCC CATCGGATCA ACTCTTCAG CTGGATAAGG	300
TCTTTTATGC AGGTATCGGC TACTTGCTTG TATTGGGAT TGTCTATAGC ATTGGTCGTT	360
TGCTTGGTCT TCTCTTACAC TTGATTCCCTA GCAAAAAACT GGGTGGTAAG TTGTTCCAAG	420
TTTCAGCAGG TATCTTGTCC ATGTTGGTGA CCTTATTGT CTTGCAAATG GCCTTGACAA	480
TCTTGGCGAC CATCCCCATG GCAGTTATAC AAAATCCTCT TGAAAAGAGT ATCGTCGCAA	540
AACACATCAT CCAGAGCATA CCGATAACAA CCAGTTGGCT CAAACAAATC TGGGTGACAA	600
ATTTAATCGG ATAAAAAGGG CAGGAGTTT CCTAGCCCTT TGTTTACAGA TTTGACTCGA	660
ATCTATCAGA ATGTAAAAAG CTACCACACC TAGACATTCA AAGACAAGGA AATAAAGATG	720
AATAAGAAAA TATTAGAAC ATTAGAGTTC GATAAGGTCA AGGCCTTGTT TGAGCCTCAT	780
TTGTTGACCG AGCAGGGCTT GGAGCAATTG AGACAG	816

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1001 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CTTGAAGCAG CTGAAAGCAT GGGGTCTTCG GGATTTAAAA CCTATTGTA ACGGGTTGTT	60
TTACCTTCC TAGTTCCAAC CTTACTAGCA GCTCCTTGCT TGTATTTATG AGAGCATTCT	120
CAGACTTTGG AACGCCATG TTGATTGGCG AAGGATATCG GACTTTCCCT GTCCTGATTT	180
ATACCCAATT TATTAGCGAG GTTGGAGGAA ATTCTGCTTT TGCAATTATG GCGATTATCA	240
TTGCCTTGGC AATTTCCCTT ATCCAAAAAC ACATTGAAA CCGCTACAGT TTCAGCATGA	300
ATCTGCTCCA TCCAATTGAG CCTAAAAAAA CTACAAAAGG AAAAATGGCT GCCATTTATG	360
CAACAGTCTA CGGAATTATC TTTATCTCTG TTTTACCTCA AATCTACTTA ATTATACCT	420
CTTTCCTAAA AACATCAGGT ATGGTATTG TTAAAGGTTA TTCTCCAAAC AGTACAAGG	480

TAGCTTCAA TCGTATGGGA TCTGCTATTT TCAATACCAT TCGTATCCCT TTGATTGCCT	540
TAGTTCTAGT TGTTCTATT TACGACATTT ATCTCCTACC TAGCCGTTAG AAAACGGAAT	600
TTGTTTACAA ACTTAATTGA CAGCCTCAGT ATGGTACCTT ATATTGTACC AGGAACCGTT	660
CTAGGGATTG CCTTCATTTC TTCCCTCAAT ACTGGTCTAT TTGGAAGTGG ATTTCTTATG	720
ATTACAGGGA CTGCTTTCAT CTTGATTATG TCTCTATCTG TCAGAAGAGATT ACCGTATACT	780
ATTCGCTCAT CTGTTGCTAG CTTACAACAA ATAGCACCAA GTATTGAAGA AGCTGCTGGA	840
AAGCTTAGGA AGTAGTCGTC TCAATACCTT TGCTAAGATT ACAACTCCAA TGATGCTATC	900
TGGTATCATT TCTGGAGCCA TCTTATCTTG GGTACAATG ATTCAAAAAC TCTCTACTTC	960
TATCCTCCTC TACAATGTCA AAACAAGAAC AATGACTGTA G	1001

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1064 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CTGGTTTGCA ATCTATTCCA ACTGAGATTAA CAGAGGCAGC AAGGATTGAT GGTGCGACTA	60
GCAAGCAAGT TTTCTGGAAC ATTGAATTGC CTTACTTGCT ACCAAGTGTC TCTATGGTCT	120
TTATCCTAGC CCTAAAAGGT GGGCTGACTG CCTTTGACCA AGTCTTGCC ATGACCGGTG	180
GTGGTCCAAA CAATGCCACA ACCTCACTTG GGCTCTTGGT TTATAACTAT GCCTTTAAAA	240
ACAACCAATT CGGTTATGCC AATGCCATTG CCGTAATCTT GTTCCCTCTTA ATTGTAGTGA	300
TTTCGATCAT CCAATTGAGA GTATCTAAGA AATTGAAAT TTAAGAGGAG AAGCATGATG	360
AAACAAGATG AAAGAAAAGC CCTGATTGGC AAATACATT TATTGATTCT AGGATCGGTT	420
CTGATTTTAG TGCCGCTCCT TGCTACCCCTC TTTAGTTCCCT TAAACCCAC TAAGGATATT	480
GTAGATAATT TCTTGGCTT TCCAACCAAC TTCACATGGG ACAACTTAG CGGTCTCTTA	540
GCTGATGGGA TTGGAGGCTA TTATTGGACT CTGTCGTCT CACTGTCTTG TCTTACTTG	600
CAGTAATGAT CTTTATCCCT ATGGCAGCCT ACTCCATCGC TCGCAATATG AGTAAAAGAA	660
AAGCCTTAC CATTGATGTA TACCCCTCTTA ATCCTCGGAA TCTTCGTACC TTTCCAAGTC	720
ATCATGATTC CGATTACGGT TATGATGAGT AAACTCGGTT TGGCTAATAC CTTGGTTTG	780
ATCTTGCTCT ACTTGACCTA TGCGATTCCA CAGACCCTCT TTCTCTATGT TGGATATATC	840
AAAATCTCGA TTCCAGAAAG TCTGGATGAA GCAGCAGAGA TCGATGGGGC TAATCAATTT	900
ACAACCTATT TCCGCATCAT NTTCCCAATG ATGAAACCGA TGCATGCGAC AACCATGATC	960
ATCAATGCC CTTGGTTCTG GAATGACTTC ATGTTGCCAC TCCTTGCTT GAACCGGGAT	1020
TCCAAAATGT GGACTCTGCC TTTGTTCCAA TACAACCTACG CAGG	1064

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 586 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CTGTAAAAGA	AGTTAATCAA	GTTGATAAAG	CACTTTAAA	ACAAATTGGT	GCAGTTGATG	60
TCTTAGAAGT	GAAGGGTGGC	ATTCAAGCAA	TCTATGGAGC	AAAAGCAATC	TTATATAAAA	120
ATAGTATTAA	TGAAATTTA	GGTGTAGATG	ATTAAGTACT	TACTGACTTA	ATAAAAAAACA	180
GAGGAGAGTG	ATGGATGAGT	AGGATGAAAT	GAAATCGCAT	ACAAGAAAATA	AAGAACTCAT	240
TATCCAAGTT	GGATACGCTT	ATTACATAGG	AGAATACAAA	TGAAATTAG	AAAATTAGCT	300
TGTACAGTAC	TTGCGGGTGC	TGCGGTTCTT	GGTCTTGCTG	CTTGTGGCAA	TTCTGGCGGA	360
AGTAAAGATG	CTGCCAAATC	AGGTGGTGAC	GGTGCCAAAA	CAGAAATCAC	TTGGTGGGCA	420
TTCCCAGTAT	TTACCCAAGA	AAAAACTGGT	GACGGTGTG	GAACTTATGA	AAAATCAATC	480
ATCCAAGCGT	TTTGAAAAAG	CAACCCAGAT	ATAAAAGTGA	AATTGGAAAC	CATCCACTTC	540
CAGTCCAGTC	CTGAAAATC	ACAACAGCCA	TCCGAAGCAG	GAACAG		586

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TGGTAGTTCT	TCCTAGTGCA	GGGGCTGTAG	ACCCAGTTGC	GACCCTAGCG	CTGGACTAGT	60
CGAGAGGGTG	TTGTTGAAAA	TGGATGGNTA	TCGCTATGTT	GGTTATCTAT	CAGGTGACAT	120
CCTCAAAACG	CTTGGCTTGG	ACACTGTTTT	AGAAGAAACC	TCAGCAAAAC	CTGGAGAGGT	180
GACTGTAGTC	GAAGTTGAGA	CTCCTCAATC	AACAACAAAT	CAGGAGCAAG	CTAGGACAGA	240
AAACCAAGTA	GTAGAGACAG	AGGAAGCTCC	AAAAGAAGAA	GCACCTAAAA	CAGAAGAAAG	300
TCCAAAGGAA	GAACCAAAAT	CGGAGGTAAA	ACCTACTGAC	GACACCCCTTC	CTAAAGTAGA	360
AGAGGGGAAA	GAAGATTCAG	CAGAACCATC	TCCAGTTGAA	GAAGTAGGTG	GAGAAGTTGA	420
GTCAAAACCA	GAGGAAAAAG	TAGCAGTTAA	GCCAGAAAGT	CAACCATCAG	ACAAACCAGC	480
TGAGGAATCA	AAAGTTGAAC	CACCAAGTAGA	ACAAGCAAAA	GTCCCAGAAC	AAACCGTGCA	540
ACCTACACAA	GCTGAGCAAC	CAAGTACACC	AAAAGAATCA	TCACAACAAG	AAAATCCTAA	600
AGAAGATAGG	GGAGCGGAAG	AGACACCGAA	ACAAGAAGAT	GAACAGCCAG	CAGAAGCCCC	660
AAGAAATCAA	GGTTGAAGAA	CCAGTAGAAT	CAAAAGAGGA	GACTGTTAAT	CAACCTGTTG	720

AACAACCAAA	AGTGGAAACG	CCTGCTGTAG	AAAAAACAAAC	GGAACCAACA	GAGGAACCAA	780
AAGTTGAAGT	AACAAGTATT	CCCCAAACTA	CTCGCTATGA	GGAAGACCTT	ACTAAGGAAC	840
ACGGAACGCG	TGAAGTTGTT	AAGGAAGGTA	AGAATGGCAG	TAGAACAGTT	ACTACTCCAT	900
ATATCTGAA	TGCGACAGAT	GGTACGACTA	CAGAAGGCAC	TTCGACAAC	GATGAAGCTG	960
AGATGGAGAA	AGAGGTTGTT	CGTGGTGGCA	CGAAACCAA	AGAAAAATT	GCTCCAGTCT	1020
TAAGTTGAC	AAGTGTACAA	GATAATGCAA	TGTTGCGTAG	TGGCAGACTT	ACTTATCATT	1080
TGGAAAATAC	AGATAGTGT	GATGTGAAA	AAATTCA	TGAAATTAAA	AATGGCGATA	1140
AGGTTGTCAA	AACTATTGAC	TTATCTAAAG	AGAGATTATC	AGATGCTGTT	GACGGTCTTG	1200
AACTTTATAA	AGATTATAAAG	ATTGTGACGA	GTATGACCTA	TGATAGAGGT	AATGGTGAAG	1260
AAACCTCTAC	GTTGGAAGAA	ACTCCACTAC	GATTAGACCT	CAAGAAGGTT	GAATTGAAAA	1320
ACATCGGCTC	TACTAATCTC	GTCAAAGTAA	ATGAGGATGG	TACTGAGGTG	GCAAGTGACT	1380
TCTTAACAAG	AAAACCTGTG	GATGTGCGA	ATTACTACCT	CAAAGTA	TCCCGTGATA	1440
ATAAAAGTTGT	TTCCCCTCCC	AGTTGAAAAA	ATTGAAGAGG	TGACTGAGGA	AGGTCCACCA	1500
CTTTACAAAG	TCCCTGCTAA	GGCCCTAATT	TGAT			1534

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 695 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CGGATTGTT	TATCTCAAGA	AGAGTCGCGA	TATTCTCCGT	GAAAGTTCAAG	AATTGATTAN	60
CCAAACGGTA	GAAGATTATC	TTCAAGGAGA	TGACTTTGAC	TGGGCAGATC	TTAAAGGGAA	120
GGTCGANAT	AATTGACCA	AGTATCTCTT	TGACCAAACC	AAGCGTCGTC	CANCTATTTT	180
ACCAGTAGTC	ATGGAAGCAA	AATAATCGTT	GAAATAAACAA	GAGAGAAAGT	CGAGTTTCGG	240
CTTTTTCTTA	TAGAAAAATA	GAAGGGAGAA	ATCATGGCAG	TAATGAAAAT	CGAGTATTAC	300
TCACAAAGTAT	TGGATATGGA	GTGGGGGGTG	AATGTCCCTCT	ACCCGTGATGC	CAATCGAGTG	360
GAAGAACCAAG	AGTGTGAAGA	TATTCCCCTC	TTGTACCTTT	TGCACGGGAT	GTCTGGAAAT	420
CATAATAGTT	GGCTTAAGCG	GACCAATGTA	GAACGCTTGC	TTCGAGGAAC	TAATCTCATC	480
GTTGTTATGC	CCAATACCAAG	CAATGGTTGG	TACACCGACA	CCCAAGTATGG	TTTTGACTAC	540
TACACGGCTC	TAGCAGAGGA	ATTGCCACAG	GTTCCCTGAAA	CGCTTCTTCC	CTAATATGAC	600
TAGCAAGCGT	GAAAAGACCT	TTATCGCTGG	TCTTTCTATG	GGAGGCTACG	GCTGCTTCAA	660
ACTGGCTCTT	ACGACAAATC	GTTCCTCTCA	TGCGAG			695

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1096 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CTCATCCAAG AATAGCATAA AAGAACTCTT CTGTTTTTC TTGAGGAACG AGAAAGTCAG	60
CAATCTCCAT TCCACGATCC ATCAAATCCT CTAAGACAT CGTGATTTT AAAGTAGTAT	120
CACTAATTG TTTCATTTTC ATTGCTAGTA ACCTCATACT TTCAGTTCTA TCTATTATAC	180
TAGATTTTA CGATTTTATC AAAAGAAGGC TCCTCTATAC GGATAGATTT TCCCTAGGGT	240
CTTTCTATAG GAGACTCCAA GAGAAAATTT CTGCAGACAG ATAGAAAAAG CCTTCAAAAT	300
CGGCTCTTAG CCGATTTGA AGACCTTATA CATCAGAATA CTTATAATTT AAAGGTTGCT	360
ACACCGAGGA TAGAACGATT TAAGTTCTG AGAATTTGAA GACTTGCTC AAATTTCTTA	420
TAACGAATTC ACTCCGTACT CTTCAACAAG AAGGACTGTA TCTCTTCCA AAAGAGATGA	480
TACATCCTGC AAATCTACAA ATGCATTCTT TTTAAAGCTT CTTGACTCTG TTTCAATTAA	540
TCTAGGATAG CTTTATTGTA GCTAACGATG GTCAATTCTT GTCCAGTATT TTTGTATGAC	600
AAAACATCTG CTAGGTTAGC AATTGTTGTA ATCTCTGTTA CAAAATCAAT TTGATACTGA	660
GAAAAATCAC CTACTCTATT GATTGTTGGA TTAAAGAGAT AAACAAACAC ATTTCCCAC	720
ACAACCAAAA TCACACAAAC CACTCCAATA ACAACTAAAC GAAGAACAG ATTTTTCAAA	780
TTTAAGCCAA GCGCTGTTTC ACCATTGCG TTCAATTCTT TAGAGTTGAT GGTTTCCAGT	840
TTTTCAATTTC TCACATTGCA ATAAGCATGT TTAAATTTCT CAATCAACCC ATCAATTTC	900
TTCTCTAACCA AGTCATTGGC ATCTTTACTT GATGTCAAAAA TTTTCACACC AACCCCTGCA	960
TCGTCAATCA TATAGTAGAC GGTCAATTTC TTCCACCAAT AGTCATTGCT TGAATTTC	1020
AAGGTTGTTT CCGTCGTGTC TAATTCACTG GCAATTTC TCAACTCACT GGGTTCTACA	1080
TCATTGAAAA GATAAG	1096

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1037 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TCCCCATCCC AGTGGGCAGC AGCATTAGTC TGTACTTCTG CGTCGTTGCG TTTTATTAGA	60
AGACTGATTT TGCTTTGAAC TACTTGAAGC TGTCGTTGTA TCCTGCGAAG TTTTTGCTAA	120
CTTCAGTTTC ATTTGCAGCG ACATGACTAG TTGCCAAGCC TAGTAAACAG ATACTTGCTA	180
ATCCAATTTC TGTTTCAAT CTTTCCTCTC CTATAAAAAA TGTAACAGAC ATCTGAATGC	240

TGTTCCACCT	AGCTTTGCT	ACTTACTGAT	TATTTTACAA	AGTCAGCAA	AGCCAAGAAG	300
CTTTCAGCTT	CAAGTGACGC	ACCACCTACA	AGGGCACCGT	CAACGTCTGG	GCAAGCCATG	360
TATGAAGCAA	CATTTTCAGG	TTAACAGAA	CCACCGTATT	GAACACGAAC	TTTGTCTGCG	420
ACTTCTTGAC	CAAAGTCAGC	AGCTACAACG	TCACGAACAA	CTTACACAT	TTTTTGTGCA	480
TCGTCTTGTG	AAGCTGATT	ACCACTACCG	ATAGCCCAGA	TTGGCTCATA	AGCGATAACT	540
GAGGCACCAA	CTTGTTCAGC	AGTCAATCCA	GCCAATGCAG	CAGATACTTG	AGCACCTACG	600
AATTTCAGCAG	CTTACCCAGC	TTCGTAAGTT	TCAAGTGATT	CACCACAACA	GATGATTGGA	660
AGCATAACCGT	TCGCAAAGAT	TGCTTTGCT	TTTTTGTGTA	TATCTTCGTC	AGTTTCATGG	720
AACTAGTCAC	GGCGTTCTG	AGTGACCGAT	AACAACGTAG	TCAGTACCGA	TTTCTTCAA	780
AACTTGTGGG	CTAGTTTCAC	CAGTCAAAGC	ACCTGCATT	TCTCCGTAGC	AGTTTTGAGC	840
AGCGACTTTT	AAGTTTGAGC	CTTNGGAAAC	AGCAAGNACA	GTTGTCAAAT	CAAGAGCTGG	900
AGCAGNGATA	CCTGCTTCAA	CAAGATCTGA	TGAAGGAAGT	TTTGATGCAA	CTGCTTCAAC	960
GAATGNTCCA	GCTTNTTGGG	GATTTTGTT	CATTTTCCAG	TTACCAAGCGA	TAAATGGTTT	1020
ACGTGACATT	TCACATA					1037

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CTTATCGTAC	TAAGGATGGC	AGTGTCAAC	TGTTCCGTCC	TGATGAAAAT	GCTAAACGCC	60
TGCAACGTAC	ATGTGACCGT	CTCTTGATGC	CAACAAGTTC	CGAACAGACA	TGTTTGTAGA	120
AGCTTGTAAA	GCAGTTGTCC	GTGCGAATGA	AGAATACGTA	CCACCATAACG	GAATAGGTGG	180
AACTTTATAT	CTTCGCCCTC	TTTTGATTGG	TGTCGGAGAT	ATTATCGGGG	TAAAACCGGC	240
AGAAGAGTAC	ATTTTCACCA	TCTTGCTAT	GCCAGTTGGA	AATTACTTTA	AAGGTGGTTT	300
GGTCCCAACC	AACTTCTTGA	TTCAGGATGA	GTACGACCGT	GCAGCACCAA	ATGGTACAGG	360
TGCGGCTAAG	GTTGGTGGAA	ACTATGCTGC	AAAGTCTCTTA	CCAGGAAA	TGGCCAAGTC	420
ACGCCATTTC	TCAGATGTTA	TCTATCTGGA	CCCATCAACT	CATACAAAGA	TTGAAGAAGT	480
CGGATCAGCT	AATTCTTTG	GAATTACAGC	TGATAATGAA	TTTGTAAACAC	CATTGAGTCC	540
ATCTATCTTG	CCATCTATTA	CCAAGTATTC	CTTGCTTTAT	TTGGCAGAAC	ATCGCTTGGG	600
ATTAACCTCCT	ATTGAGGGTG	ATGTTCAAT	TGATAATCTT	GACC GTTTTG	TAAAGGCAGG	660
TGCCCTGTGGT	ACAGCAGCGG	TTATTTCTCC	AATTGGAGGT	ATTCAACATG	GTGATGATT	720
CCATGTTATT	CTATAGTGAA	ACAGAAGTAG	GTCCTGTGAC	ACGTAAATTA	TATAATGAAT	780
TGACGGGTAT	TCAGTTTGGC	GATATTGAAG	CGCCAGAAGG	TTGGATTGTA	AAAGTAGATT	840
AAAAATAAAC	AAAGGAGATT	TTTTATGAAA	TAGAAAAAGT	GGCTCTAAC	AGCAGGAGTG	900
GTCCTGAGCA	CGTCAGCTAT	TTTAGTGGCT	TGTGGAAAAA	CTGATAAAGA	AGCAGATGCA	960
CCGACAACAT	TTTCTTATGT	CTATGCAGTA	GATCCAGCAT	CATTGGGCTA	CA GTATAGCG	1020

ACTCGAACAT CGAGGACAGA CGTTATTGGA AATGTTATTG ATGGTTTGAT GGAAAATGAT	1080
AAATAACGGCA ATGTTGCTCC TTCTCAAAAA GACTATGATT TGAACAGTAC AGGATGGGCT	1140
CCAAGCTATC AAGATCCAGC GTCTTACTTG AATATTATGG ATCCAAAATC TGGTTCTGCC	1200
ATGAAACACC TTGGCATTAC GAAAGGAAAA GATAAGGATG TTTGTAACTA AACCTGGTTT	1260
GGATAAAATAT AAGAAATTGT TAGAAGATGC TGTTTCTGAG ACCACTGACC TAGAGAAGAG	1320
ATATGAAAAA TATGCCAAAG	1340

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CTCTGACGGC GTCGCCACTT AAGAAGAGTA TCAAAAAGAA AAATAGAAAA TTAACTAACA	60
AGGNAGAAAA ACACATGTCT AAAATTATCG GTATTGACTT AGGTACAACA AACTCAGCAG	120
TTGCAGTTCT TGAAGGAACG GAAAGCAAAA TCATCGCAAA CCCAGAAGGA AACCGCACAA	180
CTCCCATCTGT AGTCTCATTC AAAAACGGAG AAATTATCGT TGGTGATGCT GCaaaACGTC	240
AAGCAGTCAC AAACCCAGAT ACAGTTATCT CTATCAAATC TAAGATGGGA ACTTCTGAAA	300
AAGTTTCTGC AAATGGAAAA GAATACACTC CACAAGAAAT CTCAGCTATG ATCCTTCAAT	360
ACTTGAAAGG CTACGCTGAA GACTACCTTG GTGAGAAAGT AACCAAAGCT GTTATCACAG	420
TTCCGGCTTA CTTCAACGAC GCTCAACGTC AAGCAACAAA AGACGCTGGT AAAATTGCTG	480
GTCTTGAAGT ANGACGTATT GTTAACGAAC CAACTGCAGC AGCTCTTGCT TATGGTTGG	540
ACAAGACTGA CAAAGAAGAA AAAATCTTGG TATTGACCT TGGTGGTGGT ACATTGACG	600
TCTCTATCCT TGAATTGGGT GACGGTGTCT TCGACGTATT GTCAACTGCA GGGGACAACA	660
AACTTGGTGG TGACCGACTTT GACCAAAAAA TCATTGACCA CTTGGTAGCA GAATTCAAGA	720
AAGAAAACGG TATTCGACTT GTCTACTGAC AAGATGGCAA TGCAACCTTT GAAAGATGCG	780
GCTGAAAAAG CCAAGAAAGA CCTTTCTGGT GTAACCTCAA CACAAATCAG	830

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 667 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GTGGTGGTTT	GAETGCCCTT	ATCGAAGCAG	GTTTCGAANT	CTAACAGACANA	AGCAGGTTAC	60
GCTCCAGAAT	TGGCTTAACT	TTGAAGTTCT	TCACGGAAAT	GAAATTGATC	GTTGACTTGA	120
TCTACGAAGG	TGGATTCAAG	AAAATGCCTC	AATCTATTTTC	AAACACTGCT	GAATACGGTG	180
ACTATGTATC	AGGTCCACGT	GTAATCACTG	AACAAGTTAA	AGAAAATATG	AAGGCTGTCT	240
TGGCAGACAT	CCAAAATGGT	AAATTGCAA	ATGACTTTGT	AAATGACTAT	AAAGCTGGAC	300
GTCCAAAATT	GAETGCTTAC	CGTGAAACAAG	CAGCTAACCT	TGAAATTGAA	AAAGTTGGTG	360
CAGAATTGCG	TAAGCAATG	CCATTGTTG	GTAAAAACGA	CGATGATGCA	TTCAAAATCT	420
ATAACTAATT	AGAAATATAT	AGCGCTGGAG	ATGATTTAT	GAAAAAGATT	ATGAGAAAAAA	480
TTGCATCGTT	ATTATTGGTT	CTAGTTGTAT	AATGTAATTAA	CACCGTCGGT	AATAGTGCTA	540
GCAGACCAAA	ATAAACGAGA	TTGGTCGTAT	GATGAAAATA	CTGTAATTAA	CATTTATGAT	600
GATGCTAATT	TTGAAGATGG	TAGGTTGCAT	ATGACCTTTG	AACAATTCTT	CAAATTGGCA	660
CAAATAG						667

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CGGTTCCAGA	NACTGGTATG	GCTAGGAGTC	GCGACAAAGT	GTATCTTATG	ATGGTCGATT	60
TGATACTCAA	TACCGCTCAAT	ACTTACGGAA	AGAATAAACG	ATCATTGTCA	ACCGGAATAG	120
TATGATAATC	GTTCCTTGGT	GGAATAAGTT	CAATCTTATC	CTTCTTAGGC	ACAATAATGG	180
AAGAGCCCAG	TGTTCGATAAA	ACACGATTAT	TAAGGCTGGC	AATTCCGTT	AATTGCAAAG	240
CTTCAATGGT	AGGGTGTAAA	ACAGCACAC	CAAGAGACTA	GTTATAGGCA	GTACTACCAAG	300
TCGGTGTGGA	AACTGTTAGC	CCGTCTCCAC	GAAAACGTT	AAAGGGAACA	CCATTTATTA	360
CAATATCTGC	CACCATGGTT	CGATCAGACC	TGCGGATGCT	GGCTTCGTTG	AGTGCTCTGA	420
AAATCTTAAC	TTCACCATT	TCAAGAAAGA	CCTTCACATT	CAGAACAGGG	TAAGAAACCC	480
TTGCCCCAGT	ATCTAGCTGC	AAATTAGTCA	CTAGCTTGT	CAACTCAAAA	TCACGATAAT	540
CTGTATAGAA	GCCCCAAATGT	CCAGTATGAA	GACCGATAAA	GCGGACCTTG	TCAAGCTGAT	600
TTTCGTACTT	ATGAAAGGCC	GACAAGAGCA	TACCATCCCC	GCCAATGGAA	ATGACAATAT	660
CCGGATTGGT	ATCATTGAGT	TATAAACTGA	TTTCTCTTCA	AACGATCTCG	CAATTCTATAC	720
AAAACCTTT	GAECTCTGCG	TTTTCTATTG	GCTATCAGAT	CAATTGTTT	ACCTGTATTC	780
TTCATCTGTA	TCGTCACTGN	NTCCAACACC	GTCATTTAAT	TTTCTACTCA	AAGGATCAAA	840
AAAGTGCCTGG	GCTTCTTGGA	TATCATCACG	AATTTCACCC	ATTTCTTCAT	CCAACTGATG	900
GGCGATTCTA	GCTGTAATT	CCAGTCGCTT	CTTAATCTCA	TCTGGAAAT	CCCCTTGGTA	960
CTTGTAGTTG	AGAGAATGTT	CTATCGTTGC	CCAGAAATTC	ATGGCCAAAG	TACGAATTG	1020

AATTTCTGCC AAAATAGTCT TAGCTCCATT GATGGTATCA ACCGTATATT CTACTACCAC	1080
ATGATAGGAA CGATAGCCTG ATGCTTTCT ATGAGTAATG TAATCTCGCT CCTGTATGAT	1140
TCGCATATCC TGACGCTTGT GCAAAATATC CACTACTTCC TTGACGTCAT CTACAAACTG	1200
AACCATCACCA CGTAAGCCAG CAATATCCTG CAAATCGTGT TCCAAGGTGCG CATAAGTAAT	1260
GCCACGACGA GCCATTTTTT CTTTGATGCT CTCATTGGC TTGACTCGAC CGGTACACAA	1320
CTCAATTGGA GAATGCTTAT TTTGCTTACG ATATTGCTTA CGAATACACAC GAAGTTAAC	1380
CTTTAACTCA CCAACAG	1397

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CTCCCATGAC ACCTGCACGC TCCGTACGGG CCACGTGCTT TTTAATCCGT TCAACAACTT	60
CATAACCCGC TTCAACATCC ACACCCGACT GGGCATATGC ATTTTTATTT GTCATTTGTT	120
TTTCCCTTTT CTTTAATGGA GAATCTGTCG CCTACTTGTG AAAACTGGTC TTTTCTTCCA	180
AACTTCTACG ATAGTCTTCT TCGTAGTCAT AGAGAGGCGT TGGGTAGTCA CCGTCAAAGT	240
AAGCGACACA GAGACCACCG TTCGGCCGCAT CTGTTTCGAT ACCAATCGAC TCAATCAAGC	300
TATCAATTGA AAGATAAGTC AGACTGTCCG CACCAATGAT TTGGCGAGTT TCTTCGACCG	360
TATGATTGGC TGCAATCAGC TCCTGACGGG TCTGGATATC AATCCCGTAG AAACATGGAT	420
ACGCTAGTGC AGGACTTCCA ATGGCAACGT GAACCTCAGT CGCACCCGCT TCTTTCAAGA	480
GCTGAACGAT ACGACGAGAG GTTGTCCAC GTACAATGGA ATCATCCACC ATGACCAACAC	540
GTTTGCCTTT GACAACACCC GAAACAGCAG ACAGTTTCAT CCGCACTCCT TGCTCCCGCA	600
ATTCTTGAGT CGGTTGGATA AAAGTTCGCT GGGTGTATTG GTTTTGATC AGACCCATT	660
CATTTGGTAA GCCTGATTCT TCCGCAAATC CCATAGCCGC GCTTAGGGAA GAATTGGGCA	720
CACCAACTAC AATATCTGCC TCATGCTTAA ATTCTCGCGC CAATTGCGCT CCCATTCTCT	780
TACGTGCCGT ATGGACATTG ACCCGTGGAT ATTAGAATCA GGGC	824

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1020 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTTCTTCCTT	GGTACTTCCT	CAATTGGATT	ACCTTTGGCA	TTGCTAGTTT	TTCACTCCTA	60
CCTTATATCC	AAGGCACTAA	AATTATGTTT	TACCGAGCAG	TATTGGCTCG	AAAACGTCCA	120
AAAGCTTGAA	GGTTTCCCCC	TCAAGCTTTT	TTCTATCAAT	GAATTCTCC	GCCTACCAAC	180
GTGAGTTCTT	GATCTCCATG	TTCTATCATA	GCGCCGATTG	CTGCTTCTAT	CCCTCGCCGA	240
ATATCCACTA	AACTCATAGT	TGGAGTAGTC	GGTCTGTTCA	CCACCTGTT	CATCATATAA	300
GGAATATGCA	TAAAACCTGC	CTTAACATAT	GGGAATTCT	TTTCTACCAA	ATAGAGAGCC	360
TGATACATCA	AATGACTGCA	AACAAAAGTC	CCTGCACGTA	TTGGAAACAG	ACTGCCGTA	420
AGTCCTTCTT	TTTTATTAGC	TTGTACCATC	GCTTGATAG	GTAAACTACT	AAAATAGGCC	480
GATGCTCCAT	CAATACGAAT	CGGTGTATCA	ATTGGTTGAT	TGCCTTCGTT	ATCAGGTATG	540
CGAGCATCAT	CTTGATTAAT	AGCCACTCGT	TCAGGTGTTA	AGCCGGTCCT	GCCGCCTGCT	600
TGTCCAATAC	AAAGTACAGC	ATCTGGTTGA	TATCGTAATA	TTTCTGCCTC	AAAACTTCT	660
GACGACTTAT	AAAAAACCGT	TGGAATTCT	ACCCAGCGAA	CTTCAGCCCC	ATTAATCTCA	720
GATGGTAATA	ATTTTACAGC	CTCCAAAGCT	GGATTAATCT	TTTCACCTCC	AAAAGGATTA	780
AAACCTGTAA	CCAAATTTT	CATTTTATTT	TCCTTTACTA	AAATGCGAGA	AAGTACATTA	840
AGAATATGTG	AATAACAATC	ATTACTAGAG	CAACACCTGC	TTGAGCCTTT	ATAACGCCAT	900
TCTGATCTT	CATATCCATC	AATGCTGCTG	GTAGAGCGTT	AAAATTAGCA	GCCATTGGGG	960
TCAATAAGGT	CCCACAATAA	CCTGCTGTCA	TGGCAAGAGC	ACCAGCCACA	ATTGGATTAG	1020

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 600 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CTCGTAAAAA	CACTAAAGGA	GGTAAATAAC	CAATGTTAGT	ACCTAAACGT	GTTAACACCC	60
GTCGTGAATT	CCGTGGAAAA	ATGCGCCGTG	AAGCAAAAGG	TGGAAAAGAA	GTAGCATTG	120
GTGAATACGG	TCTTCAAGCT	ACAACTAGCC	ACTGGATCAC	TAACCGCCAA	ATCGAAGCTG	180
CTCGTATCGC	CATGACTCGT	TACATGAAAC	GTGGTGGTAA	AGTTGGATT	AAAATCTTCC	240
CACACAAATC	ATACACTGCT	AAAGCTATCG	GTGTGCGTAT	GGGATCTGGT	AAAGGGCAC	300
CTGAAGGTTG	GGTAGCACCA	GTTAAACGTG	GTAAAGTGAT	GTTGCAAATC	GCTGGTGTAT	360
CTGAAGAGAT	TGCACGTGAA	GCGCTTCGAC	TTGCTAGCCA	CAAATTGCCA	GTAAATGT	420
AAATTCTGAA	AACGTGAAGC	AGAATAAGGA	GAAGGCATGA	AACTTAATGA	AGTAAAAGAA	480
TTTGTAAAG	AACTTCGTGG	TCTTTCTCAA	GAAGAACTCG	CGAAGCGCGA	AAACGAATTG	540
AAAAAAGAAT	TGTTTGAACT	TCGTTTCCAA	CCTGCTACTG	GTCCAATTGG	AAACAAACAG	600

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTTCAGCGAC ATATCTATCC ACAACTTCTC TCGATTCATG TTCCCTCTGAA AATGCCTGAA	60
ATTTTAATTG ACTAATTGTA TCCTGATACG AACTATCTGC TAACAAAACT TCAAGATGGG	120
AAACATTGTC TAACGGATAA GGTCTTCTAT CCTTACCTAA CCAAGTTTCT GTCTCTTCAT	180
CCTCTATTAG TCCCCAGTTA CTGGCAAAGT CAGGATGATT CTCTAAAAAA ATACGTTCTG	240
TCTGAAAAGT GACTGACCAGA ATGGGGAAAG AAGCTGTTCC TCTCTCAAAA CTAGTAAACA	300
ATGCACGCCG AATCCCCTGA CGCGATGAC CTGGATGAAC CAGTATCGTC ACTTCTACAT	360
CTTGGTCATC TGCA TAGACA GTTAATAAAC CAACAAGTTC GCCTTTTCA TAATAAAGGA	420
AAAAGGCGGG CATGTTTGGGA TCAAAATTAA GCATGTTAGA GAGATAGGGA TCGCGATAGG	480
TACCGTCATA GTTTGGCAA CAGTTAATTAA CTTTTTTCGC CTCAGATAGC TCTTCTTGGC	540
TTAACATTGTT TCTTGCTTGA ATCATATAGG TATCCTCTAC AAACCAGACG ATCTGTGACT	600
GGCATCTTAA GCCTGCTCGA GTTTATTGAC ATAATACTCC CGTTTTCTT CGACTTCGTG	660
AATAACAGGC TCATCTTCT TACCATGAAG ACGGACAATC TTGGCCGGAA TACCGACAAAC	720
CGTCACATCA CTAGGTACAT CTGCTACGAC AACTGCTGCA GCACCGACCT TGGCATTTC	780
ACCAATTCTC ACAGGCCCGA TAACTTGGC ATGGGCTGAT ATGAGGGCTC CCTTCTGTAC	840
AGTCGGATGG CGTTTGCCAC AGTCTTCCC TGTTCCCCCG AGAGTCACTC CGTGATAGAG	900
AAGAACGCCT TTTTCAACAA TCGCTGTCTC TCCAATCACC AGACCAGAAC CATGGTCAAT	960
AAAGACACCT GAATCAATCT GGGCTCTGG ATGAATCTCA ATCTGAGTCC AAAAGCGCCA	1020
AAACTGACTG TGCA TAGCGAG CTAAGAGTTT GAAGTCGTAC TTCCAGAGAA AATGCGAGAG	1080
ACGGTGGGCC GCCAAGGCCT TGACACCTGG ATAAGTCAGC AAAACCTCCA AAGTGGTGCG	1140
GGCCGCTGGA TCATTTCTT TTACGATATC AATGGTTTCC CGCCACCA ACCATACATT	1200
CTCCTTTCT TACTCTGAAT CTT	1223

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 845 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GGTGAGTGCC	TTTATTAGCG	GAGCTTCTCA	AGTGATTGTT	GCCTTGATTA	TCTTCCTTTC	60		
ATGCTCTTTT	ATCTCTTGC	TGATGGAAA	GGCTTGC	GTA	ACTATTTGAC	CCAATTCA	120	
CCAAGCAAAT	TGAAGGAACC	TGTTGGACAA	GTTC	TATCAG	ATGTGAATCA	ACAGTTGTCC	180	
AACTATGTT	CAGGGCAAGT	GACAGTGGCT	ATTATTG	TAG	CAGTAATGTT	TATCATCTTC	240	
TTCAAGATTA	TTGGTCTACG	CTATGCCGTT	ACGCTGGGG	TTACTGCTGG	TATTTAAAT	300		
CTGGTCCCC	ATCTTGGTAG	CTTCTAGCC	ATGCTTC	CTG	CCCTAGTATT	GGGTTGATT	360	
GCTGGTCCAG	TCATGCTTTT	GAAAGTAGTG	ATTGTCTTA	TTGTAGAACA	AACTATTGAA	420		
GGCCGTTTTG	TCTCTCCATT	GATTTGGGA	AGTCAATTAA	ACATCCACCC	TATTAATGTT	480		
CTCTTTGTTT	TGTTAAC	TC	AGGATCTATG	TTTGGTATCT	GGGGAGTTT	ACTTGGTATT	540	
CCGGTTTATG	CCTCTGCTAA	GGTTGTC	CATT	TCAGCC	TCGAATGGTA	TAAGGTAGTC	600	
AGTGGTCTAT	ATGAATTAGA	GGGTGAGGAA	GTCAAGAGTG	AACAATAGTC	AACAGATGTT	660		
ACAGGCTT	TG GAGGAGCAAG	ATTTA	ACTAA	GGCTGAGCAT	TATTCGCCA	AAGCTTTAGA	720	
AAATGATTCA	AGTGA	CTTC	TGTATGAGTT	GGCAACTTAT	CTTGAAGGGA	TTGGTTCTA	780	
TCCTCAGGCC	AAGGAA	ATT	TT	ACCTGAAA	AT	TGTAGAAGAT	TTTCCAGAGG	840
TCTAG								845

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CTATGGATTA	ATCTTCTTCT	ATCTTATCCT	GTTCCTAAAT	ATGTTGGTAG	AAAAATGAAG	60	
CAGTTGTTAC	GAGTGTCTGT	ATTGGAAAAA	AATTTGTCT	ATACAATTCT	TTAAATGATA	120	
TGAAGACTAG	GAATGCCAAA	ACACTGACAT	ATTCGTTTA	AAGCCTATCC	AGTCTCTCA	180	
ATTGTATTTG	TAGAAATGCT	ATCAGTAATA	TATTCGCGAA	CACTATGATT	TACAACAGTG	240	
TGGTCGTACA	TCTTGTAAC	TTTATTATAC	AACAACCATT	TACAGGTGTA	AAGTTGAGCA	300	
GTTGCTTTAG	TAAATTTAGG	GACTGTTTT	GTCATAGTTT	TGATACCTGT	ATTCGTTGTT	360	
TCATGAGTAT	TTGACGTTTC	TTTCATGTA	GGCATTCAA	CAATTAGAAT	GATATTTTC	420	
CGAGGATGAA	CTTATATATT	ATGACTTTT	AGAGTTATGA	TGCCTCTTGA	TTTGACTATC	480	
GCTATCAATT	TCATCCACTT	TTACAGTTTC	ATGCAACATA	GCGAGAAGGC	GGTTTCCTAT	540	
ATGGAAGTCG	TCTTGT	TTTC	ATATTGTCTA	AATACGAGAT	ATTTACTACA	GGTTGTAGAT	600
ATTGCAAGCT	CAAATGATAT	TATTTAGAG	GAGGAGACAA	GTGAAATAAT	GCCTGGTGAG	660	
TTAGATGAAA	AAAAAGTAA	GGAGTTGAAA	GTACTGGTTC	NTTGTGCAGG	GTCTGGAACA	720	
AGTGC	GAAT	GC	AATTAA	CCGAG	GGCGCTCNAT	TAGCAGAAGT	780
CGAATTCA							802

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CTGGGACTCT CTTCGTAGAA GTCATGCAAG AATATTTGA TCAAAAGAGG AAATCATGAA	60
AAAAAGAGCA ATAGTGGCAG TCATTGTACT GCTTTTAATT GGGCTGGATC AGTTGGTCAA	120
ATCCTATATC GTCCAGCAGA TTCCACTGGG TGAAGTGCGC TCCTGGATTC CCAATTTCGT	180
TAGCTTGACC TACCTGCAAA ATCGAGGTGC AGCCTTTCT ATCTTACAAG ATCAGCAGCT	240
GTTATTCGCT GTCATTACTC TGGTTGTCGT GATAGGGGCC ATTTGGTATT TACATAAAACA	300
CATGGAGGAC TCATTCTGGA TGGTCTGGG TTTGACTCTA ATAATCGCGG GTGGTCTTGG	360
AAACCTTATT GACAGGGTCA GTCAGGGCTT TGGTGTGGAT ATGTTCCATC TTGACTTTAT	420
CAACCTTGCA ATTTCAATG TGGCAGATAA CTATCTGACG GTTGGAGTGA TTATTTTATT	480
GATTGCAATG CTAAAAGAGG AAATAAATGG AAATTAAAAT TGAAACTGGT GGTCTGCGTT	540
TGGATAAGGC TTTGTCAGAT TTGTCAGAAT TATCACGTAG TCTCGCGAAT GAACAAATTA	600
AATCAGGCCA GGTCTTGGTC AATGGTCAAG TCAAGAAAGC TAAATACACA GTCCAAGAGG	660
GTGATGTCGT CACTTACCAT GTGCCANAAC CAGAGGTATT AGAGTATGTG GCTGAGGATC	720
TTCCGCTAGA AATAGTCTAC CAAGATGAAG ATGTGGCTGT CCTTAACAAA CCTCAGGGAA	780
TGGTTGTGCA CCCGAGTGCT GGTCAATCCA GTGGAACCCCT AAGTAAATGC CCCCCATGTA	840
TCATATTAAG GACTTGTGCG GTATCAATGG GGTTCTGCCT CCANGGATTG TTCACCCGTA	900
TTGATAAGGA TACGTCACGT CTTCTCAT	928

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CTCTTTACA GAGGTGTTTC CTATTTGTG CTTCCATTT TGGGGCAAGG AATTGTAGAT	60
GGGGATGGCA ATCCTATCTT TTTATTGATT ATGATATTG TTTGCTTCAT AGTTTTAGTC	120

TTTTTGAAAT GGTTAGACTA TGATTTCACT AGATTGAGAA GGGAGTTCT AGATACAGGT	180
TTTCAAAAGT CTCTTACTAA GATTAACCTGG GCAATGGGG CTTATTATCT AGTGATGCAA	240
AGTCTATCTT ACCTTGAATA TGAACAAGGT ATTCAATCAA CGACTGTTCG CCATCTCATC	300
CTAGTGTTC ACCTACTCTT TTTTATGGGG GGTATCAAGA AATTGGATAC CTATTTGAAG	360
GAAAAAACTTC AGGAGGAACG GAACCAAGAG CAGACCTTGC GCTACAGAGA TATGGAACGC	420
TATAGTCGGC ATATAGAGGA ACTTTACAAG GAAATTGCGA GTTTTCGCCA TGACTACACT	480
AACCTCTTAA CCACCTACGT TTGGGCATTG AAGAGAAGGA TATGGAGCAG ATAAAAGAGA	540
TGTACGACTC GGTCTTAAGG GATTCCAGTC AGAAATTGCA GGACAATAAA TATGACCTGG	600
GCAGATTGGT GAATATTNGT GACCGTGCCTC TCAAGAGTCT CCTAGCTGGA AAATTTATAA	660
AAG	663

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 653 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CTAGATTAAT CTGATATTTC TTTTGCGAA ACCAAATGCT TCCTATCAGA AAAGCTAGCA	60
ACAGCAACAT GGTAATAATG ATATGAATGG TCATTTCTT CTCCTATTCT GCCTTTCAA	120
TATCTTTTT CATCTCGTCA ACATTGAACT TAGCAAACAA GTATTGACGG TCTTGGACTG	180
GGAAACGTTG GTCCAACCTGG TCAACTGCTC CCACCTCGAT AATGCCCTCC TTGATGACAA	240
AATCCATGAC ATGTCCACCG AAGGTCAAAT CATCTGATAT GAACTGCAGA TGGTAGCCTG	300
CCACACTGAC CCCATGGAAA ATCTCAGGCG TCCAGAAACC ACAATAGTC CCCGCAACAT	360
TGTCACGACT ATATTCCGGT TGATGGGTTG CGACATCAGC AAACCTGGTA TCGGGGTGTTG	420
ACTTAGGAAT CATAACGCACA TGCATATGTT AAAAATTCCC CCCCCGAATCT TGATAGAGCG	480
AAAAAGATT TCCCCATCAT AATAAGACTC AATTCTGTTCT TTCAATTCCCT TGTCTGTCAT	540
CTCAAAGCGC TGGCGAAAAA TGACCTCTGC CTGATGCGGT ACCACTGCAG CGTAAGGAAT	600
AAGGGCATTG GGTGACACTT CCACAATTTC TGGCTGGTCT CCTGACCCCTT TGG	653

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 989 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CTACGATATC TTTGGTCTTT TGTAAGATAT GAGGTCCACC CTTATGCGCC TCAGTTGGCA	60
TTTCATGCGA TTCAAGAAAGT TGCCCCCTCTT GATCAACCAA ACCATACTTG ATGTTGGTTC	120
CACCGATATC AATTGCAACG TAATATGTCA TAAATACCTC CTTTAGATT AGAGGAAGCG	180
CTCCTTGGTT TCACGAATCA AGGCAGCAGC CGCTTCTACA ACTGGACGAT CTTCTTCAGT	240
CACTGGTGTC AATGGTGAAC GAACAGATCC AATATTCAAG CCTTCATTGA TTTCAAGAC	300
TTCTTGTAG ACACCGTACA TATTTCCATG AGCAGAAGTG AGTTACCAA TGATTGCGTT	360
GATAGCATAc TGCAATTCAc GCGCTGTTc TAGGTCTTA TCCGCAATCA ACTGATTGAG	420
TTTCAAGAAG AGTTCTGGCA TAGCACCATA AGTACCCACCG ATACCAGCCC TAGCCCCAT	480
GAGGCGTCCT CCTAGGAACT GCTCATCAGG ACCATTAAAG ACGATATGGT CTTCTCCACC	540
AAGGCTGACA AAGGTTGGA TATCTTGAAC TGGCATAGAA GAGTCTTCA CACCGATAAC	600
ACGAGGATTT TTCAACATT CTGTGTAAAG GCTTGGAGTC AAAGCAACCC CTGCCAATTG	660
AGGAATGTTG TAAATCACGT AGTCTGTGTT TGGAGCTGCA GAACTGATAT CGTTCCAGTA	720
TTTGGCAACT GAGTTATTCT GGCAAGCGGA AATAAATTGG TGGAAATCCGT TGCAATAGCA	780
TCTACTCCCA AGCTTCAGC ATGGCGAGCA AGTTCCATAC TATCTTGT ATTATTGCAA	840
GCAACATGGG CAATAATGGT CAATTTACCT TTGGCTACCG CCATGACTTC TTCCAAAATC	900
AACTTGCAGT CTTCAACGCT TTGGTAGATA CATTCAACCAG AAGAACCAATT GACATAAGAC	960
CTTGAACACC TTTATCAATG AAGTATTGA	989

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1671 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TCAAAGAGTA ACAAAAGGCAC CAAATTCTCG ATAGGAACGA TTTAGCACGG TAAACTTCAT	60
CCACTTGGGT TCACGGAACC AAACCAGCAA TAATTTCTTT GGGCACGGGT TAATAGCATT	120
TTGGTCAACT AGGAGTAGAT AGAACACATT TCNTTCTTCG TCTATATCAA TCTTAACACC	180
TGTTTCAGCG ATAATCTTGT CGATGGTTTC TCCACCCCTTA CCGATGACAA TCTTAATCTT	240
GTCCACATCA ATCTTGATCG TATCAATTCTT CGGAGCAGTT GGAGCCAATT CTGGACGAAC	300
TTCTGGAATG GTTGCTTCAA TGACATCAAG GATTCAAAA CGCGCTTCT TGGCTTGAGC	360
AAGAGCCTCC GTCAAGATTCT CGCAGTAAT CCCTTGAATC TTGATATCCA TTTGAAGGGC	420
TGTAATCCCA TCACGAGTAC CTGCAACCTT GAAGTCCATA TCTCCAAAGT GATCTTCCAA	480
ACCTTGGATA TCTGTCAATA CTGTGTAGTT ATTTCCATCT GAGATAAGTC CCATAGCAAT	540
ACCAAGCTACT GGCGCCTTGA TTGGCACACC ACCAGCCATA AGGGCAAGAG TTCCCGCACA	600
GATAGAAGCT TGAGATGAAG AACCGTTGA TTCCAAAATCTCTGACTA GACGGATAGC	660

GTATGGGAAT TCTTCCAAGC TTGGCAAGAC TTGAGCAAGA GCACGCTCAC	CAAGGGCACC	720
GTGACCGATT TCACGACGAC CTGGCCACC GTAACGACCT GTTCCCCTA	CAGAATATTG	780
AGGGAAGTTA TAGTGGTGCA TAAAGCGTTT CTTGTACTCT GGATCCAAAC	CATCAATGAT	840
TTGAGTTCT CCCATCGGAG CCAAGGTCAA GACTGAAAGA GCTTGAGTTT	GCCCCACGG	900
AAAGAGACCT GAACCATGTT ACACGAGGAA GGAAGTCAAC AACCGCATCC	AAAGGACGGA	960
TTTCATCGAC CTTACGACCA TCAGGACGCA CCTTGTCTTC TGTAATTAAA	CGTCGCAC	1020
CTGCGTGTTC CATTGTTCC AAGATTTCAG CCACATCACG CATAATACGG	TCAAATTCTT	1080
CGTGGTCCCG ATATTTTCTC TCGTAAACGG CAGTCACTTG GTCTTCACT	GCTTGAGTTG	1140
CAGTTCACCG GAATCCAATT TCTCTCTAC TTGAAC TGCC TTTGGAGGT	CACTGTTGTA	1200
GGCTGCAATG ATTCAGCTT GCAATTCAAGC ATCCACGTGA AGCAATTCCA	CTTCTGCTTT	1260
TTCTTTACCG ACAGCAGCAA CGATTTCTTC TTGGAAGGCA ATCAATTCTT	TGACAGCTTC	1320
GTGCCCTTA AGAACCGCTT CCAACATGAT TTCTTCTGAC AATTCTTGG	CACCAAGACTC	1380
TACCATGTTG ATAGCGTGC TGTTCCAGC TACTGTCAAT TCAAGAAGAG	ATTGCTCTGC	1440
TTGTTCTTGA CTTGGGTTGA TGATGATTG GCCATCTACA TATCCCAC	TT GTACCCAGC	1500
AATTGGTCCG TCAAATGGAA TATCTGAAAT AGACAGTGCC AAAGATGAAC	CAAACATAGC	1560
AGCCATTGGT GCAGATGCAT TTTCATCATA AGAAAGCACT GTATTGATGA	CTTGGACTTC	1620
ATTACGGAAA CCTTCCGCAA ACATAGGACG AATCGGACGG TCAATCAAAC	G	1671

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CTCAGTATCT TTGTAATCAA CATATCCAAT TTTGTTGCT GCGATGTANT	CAA CTTTTT	60
ACGGCGTTTG AATCCGCCAC GACGTNGTTG AGCCATGTTT TTNCCTCTT	ATAAGTTTAG	120
TTGTCCATTA GAATGGTAAA TCATCANCTG AAATATCCAA TGGTTTGT	T GCTCCAAATG	180
GATTTTCATT ACGTAAAAG TCTGGTACTG AATTGTAGG TGCTGAATAG	TTTGCAGTTG	240
GTGCAGAGTA AGCTCCACCT GTGTGACCT CACGCACACT ACGGCTTCC	AA CATTGGA	300
AATTCTCAGC CACGACCTCT GTCACGTAGA CACGTTGTCC TTGCTGGTTA	TCGTAACTAC	360
GAGTCTGGAT ACGACCTGTC ACCCCGATAA GTGAGCCTT TTTAGCCCAG	TTAGCAAGAT	420
TTTCAGCCTG TTGGGCCAC ATAACGACAT TAATAAAATC AGCCTCACGT	TCACCATT	480
GACTCTTAAA TGTACGGTTT ACTGCAAGAG TAAAAGTCGC AACTGCTACA	TTTGATGGGG	540
TATAACGCAA CTCAGCGTCA CGTGTACATC GCCCTACAAG TACAACATTG	TTAATCATAG	600
TTTACCTTCT TACGGTCAA TTTTGACGAT CATGTGACGA AGAATGTCAG	CGTTGATTTT	660
GGAAAGACGG TCAAACCTT TAGAGAGCTG CATCGNTCAT TTGCTCAAC	GTAAACGATG	720
TGGTAAAGTC C		731

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 992 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CTGGGTTTTA CCACGTTTC CTGATGTACG AGCGAGATCC TTACGGTCA ACATAGTGTT	60
GATAAAGCTG GATTACCAA CATTGAACG CCCTGCTAGG GCAATCTCTG GCAGTTCATC	120
CTGCGGATAG TGGGACTTAT TAGCTGCCT GAGCAAGATT TCAGCATTGT GTGTATTAAG	180
TTCCATAGTC ACCTCTAGGC TGTTCTAGG ATCGGTTTAT CCGTCCATC GACAGTTCT	240
TTAGTGATGC GAACCAATT CACATTTCC TGACTCGGCA CCTCAAACAT AACATCTAGC	300
ATGGTTCTT CGATGATGGA GCGAAGTCCA CGCGCCCCCTG TCTTCCGTTG GATTGCTTTA	360
TTAGCAATCT CTTGAAGGGC TTCGTCGTC AATTCCAAT CAACATCATC ATAAGAAAGC	420
AAGGTTTGGT ATTGTTTCAC CAAGGCATTT CTTGGCTCTT TCAAGATGCG AACCAAGTCC	480
ATCAACGGAC AATTGCTCAA GAGCCGAAA AACAGGCAAG CGTCCAATCA ACTCAGGGAT	540
AATACCAAAT TTTTGAATGT CTTCAGCGAT GAATTCTTGC ATGTATGAGC TGTTTCTCTG	600
TCAATCGCCT TATTGTTTG ACCAAATCCG ATGACTTTT CACCCAGACG TTGTTTGACA	660
ATTCTTCAA TACCATCAAA AGCACCAACC ACGATGAAGA GGATATTTT TGTATCCACT	720
TGAATCATCT ACTTGTGTTG GATGTTGCG TCCACCTTGA GGCGGCACGC TAGAACAGT	780
TCCCTCAATA ATCTTGAGAA GGGCTTGTG CACCCCTTCA CCAGAAACAT CACGTGTGAT	840
AGACACATTC TCACTCTTCT TGGCAATCTT GTCAATTCA TCCACATAGA TAATGCCACG	900
CTCTGCACGT TCGATGTTAA AGTCAGCAAC CTGCAAGAGT TTGAGGAGTA TATTTCCAC	960
ATCCTCACCC ACATAACCAG CCTCCGTCAG AG	992

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ATTTTCACAG GGCAGGATGC GGAACGACTA GCCCCATACT TTAACGGAAT TTTGGTAGGG	60
ACAGCTCTTA TGCAGGCAGA AAATGTGGCC CAGAGAATCA AGGAGTTGCA GATTGACAAA	120

GGTTAAAATT TGTGGACTAT CGACCAAAGA AGCGGTGGAA ACAGCCGTTT CAGCAGGAGC	180
CGACTATATC GGTTTGTCT TTGCACCTAG TAAAAGACAG GTGACTTTAG AAGAGGCAGC	240
TGAGTTGGCA AAGCTTATTTC CTGCAGATGT GAAAAAGGTT GGAGTATTTG TTTCACCAAG	300
TCGGGTAGAA CTGCTGGAAG CGATTGACAA AGTTGGCTTG GACTTGGTTTC AAGTTCACGG	360
TCAGGTGGCA GATGATTAT TTGAGAATT GCCTTGTGCC AGTATTTCAGG CTGTGCAGGT	420
AGATGGAAAT GGGCATGTCC CCAATTCTCA GGCAGATTAT CTACTCTTG ATGCCCTGT	480
GGCAGGAAGT GCCCAGTCCT TTGATTGGG TCAACTGGAT ACGACTGGAC TAGCACAGCC	540
CTTCTTATC GCAGGTGGCC TTAATGAAGA TAATGTAGTA AAAGCAATT AACATTTAC	600
TCCCTATGCA GTAGATGTAT CGAGCGGAGT GGAGACAGAT GGACAAAAAG ATCATGAAAA	660
GATTAGAAGA TTTATAGAGA GGGTAAAGCA TGGCATATCA GGAACCAAAT AAAGATGGAT	720
TTTACGGAAA ATTGGCGGA CGTTTGTCC CAGAACATT GATGACAGCA GTTTGGAGT	780
TGGAGAAGGC CTACCGTGAA AGTCAGGCAG ACCCAAGTTT CCAAGAGGAA TTAAACCAAC	840
TCTTGCGCCA GTACGTAGGA CGTGAAACTC CTCTTTACTA CGCAAAAAAC TTGACCCAGC	900
ATATCGGCGG AGCCAAGATT TATCTAAAC GGGAAGACCT TAACCATAACA GGAGCCCACA	960
AGATTAACAA TGCCCTAGGA CAAGTTGGC TTGCCAACG CATGGGTAAA AAGAAAATTA	1020
TCGCAGAAAC GGGTGCTGGT CAGCACGGTG TGGCAACTGC AACTGCTGCG GCCCTCTTTA	1080
ACATGGAATG TACCATCTAC ATGGGTGAGG AAGATGTCAA ACGCCAAGCC CTCATGTGT	1140
TCCGTATGGA GCTTTGGGA GCTAAGGTTG AAGCAGTGAC AGATGGTTCG CGCCTGCTCA	1200
AGGATGCGGT CAATGCAGCC CTTCGTTCAT GGGTGGCTAA TATCGACGAT ACCCACTATA	1260
TCCTTGGTTC TGCCTTGGGG CCTCATCCAT TTCCAGAAA	1299

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1078 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CTGTTGAATC AACAAACACGT ATCCAAGTAT CAGNATCAAA TTATGCAGGT AATCGTACAA	60
TTGGAAATCA CCGTGGATGG TTCAATCCAA CAACAACTTC TGAAGGTTTT GTTACATATA	120
TTTATGCAGA TTAATTTACA GAGGGACTCG AATAGAGCCC TCTTTTCAGG TTTTACCGTG	180
ACAATCCCTA TTAAAAATTA TATCAAATAA GCTTGAAAAT ATTGGAAAAG TATGGTAGAA	240
TGAAAATTGT CGTGTGAACG ATAATACTCA TTCTTGATGA ATTGTGAAGC AGTTGCCCTT	300
GGGTCGTTTT GCGAGTTGAA GTCAAGAAGA GGAAAAAAAC AAAAAGGAGA AATACTCATG	360
GCAGTAATT CAATGAAACA ACTTCTTGAG GCTGGTGTAC ACTTTGGTCA CCAAACCTCGT	420
CGCTGGAATC CTAAGATGGC TAAGTACATC TTTACTGAAC GTAAACGGAAT CCACGTTATC	480
GACTTGCAAC AAACGTAAA ATACGCTGAC CAAGCATAACN ACTTCATGCG TGATGCAGCA	540
GCTAACGATG CAGTTGTATT GTTCGTTGGT ACTAAGAAAA CAAGCAGCTG ATGCAGTTGC	600
TGAAGAAGCA GTACGTTCAAG GTCAATACTT CATCAACCAC CGTTGGTTGG GTGGAACCTCT	660

TACAAACTGG GGAACAATCC	AAAAACGTAT CGCTCGTTG	AAAGAAATTA AACGTGGATG	720
GAAGAAGATG GAACTTCGA	AGTTCTCCT AAGAAAGAAG	TTGCACCTCT TAACAAACAA	780
CGTGCACGTC TTGAAAATT	CTTGGCGGT ATCCGAAGAT	ATGCCTCGTA CCCCAGATGT	840
GATGTACGTA GTTGACCCAC	ATAAAGAGCA AATCCGATGT	TAAAGAAGCT AAAAATTGG	900
GAATCCCAGT TGTAGCGATG	GTTGACACCA ATACTGATCC	AGATGATATC GATGTAATCA	960
TCCCAGCTAA CGATGACGCT	ATCCGTGCTG TTAATTGAT	CACAGCTAAA TTGGCTGACG	1020
CTATTATCGA AGGACGTCAA	GGTGAGGATG CAGTAGCCGT	TTGAAGCAGA ATTTGCAG	1078

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CTATGAGGGA TATAAAGTGA	GAGAGTTGGG CCAACGTTCC	AAAAACGTCC TAAATTCTGC	60
CCATTGACAA AGGCAACCCC	CTTACCAAAAC TCAGACNAGT	CTAGGTAAGT ATCTTTGGC	120
TATTCGACTG TAAAGTCATA	AGCGTAAAAG GCTGGTTGTC	CTTGAGTCCA TCCTTTGGAA	180
AAATCAATT TCTCAGGATT	GTCTAGTGGG AGTGGATAGT	GTTTCCAGTT TAGTAAGAAA	240
TGCAGATCCT TACAGACCCC	TGTCCGAATT CCCTTACGTT	GCGTATCCGC TAAGAACTTA	300
TGCCCATAGT TGACACGCC	CATATTTCT ATCAAGATAT	CTAACCTAGA TAGCCCTTTC	360
TTTTTACCTT GATAAAAAT	ATCTTCCCCA ATCTCTGTCT	GATATTGAGT TTTAACCCAC	420
TGACCATCGA CATACAGCTG	GGCCCTATCT CGACCATCAA	TGATACGAAG TCTTTCTTCT	480
TCTGCATCCC AGTTGTTTC	TGTCGATAA AGTAGGTAGC	CATAACTTTG TCCCAGCTCC	540
TCCATTTT GAGGATAGAG	ACTTTCTACA GGGACTTGAC	AAGCTATCTA AGGTTTCAA	600
CAAAGAAACT TTTCAACTA	GTGGAATAGC ATCCAACCTCC	ATACTCTCTT TGTAGAGTGG	660
TTCCAACCTGC GGATACTCTG	AAAAATGTGT TGCCATCATC	TTCTTGACTG CAAGATATT	720
AGCAGTTGGA TTTCCTCTT	CATCCAGAAG GGCATCGTAA	TCATAAGACG TAAACTTGTG	780
GCAGGTCCAA ATTCCCTCGAG			800

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 769 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CTCACGCAGT TCTGTTACCA AAGACCGTTC	AAAAAGCAAA CTAGCAATAC TTATAACTTA	60
TTAGAAATTCTAATTTTAC CTTGCTAAAC GAATACAGGT	CACGATGCCA TCTGAGTCTG	120
TGATTTCCAA TTGGCTCGAT GTCATCCATT TGATTGGTAC	GTCAACTTCT TGTGCTCGTT	180
GGGCAATCGT TAACAGTTCT TCTTATGTG CAACTTCGAT	GACATAGTAG GCTAAACCTG	240
GTAAGCCTTG CTTACGCGGA AGCCAGACCT	TTTCCTTCCC CATTCGTTAA CTGCTAAATG	300
ATGATGGTAA TCTCCAGCCG CAATCCA ACT AGCGCCAGGC	ACACTGAATT TATTCTCTAG	360
CCCTAACACC TTTTGATAAA ACTGGCTGGA CTTTCGACTA	TCCTTGACGG AAAGATGAAT	420
ATGCCCTATT CTTGTACCTT CTGCCAGGAT AAAGGGCTCT	ACTCTTCCC CCAACTCATA	480
AATGTCCTGC GCCGCAAGAG CCTCCGTCAC TCCGATAATG	CGTCCATCTT CTCGAATATC	540
CCATGTGGAA ACTGGCTTAT CTCGATAGAG TTCAATGCCA	TTTCCCTCCA AATCTTCCAA	600
GTAAAATAGCT TCACGTAAAC CATGGTCTGC ACCGCCGACA	AGAGGAATTT GCAAATCTGT	660
CAGATGTTTC AAGACATCAG CCAAAGCCTT GCGTGTGGGC	AAGAGAATGG CCAAATGGTA	720
AAGACCATAA TGTTCCCTCA CTTCTCCGCT CTTCTTGTGC	TTGAATCAG	769

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TTACCCCCAAG CCTGCAACTT CCCAAGCTGA TTGGTTGAAT GATTTGTCAT	CAACACCACC	60
AGTATCAGTG ACGATTGCTG CTTTTGCTT CACATCAGAA GATGAAGCTG	CGTTACGAGA	120
AGAGCGGTTA CCACATGCAG CAAGTCCAAC TGCTGCCACT GCAACTAGGC	CAAGACCTAG	180
CCATTGTTTC TTGTTCATTA CTGAAACCTCC TAAATAAGAT GTGCAACGAT	GTTGCAAGTA	240
TGGATTGATT GGTCACAAAG ACCCTGCCA CTCAAAGAGC GACTCAGACT	AATTAAAGTC	300
TGTAAAAGAA TATGGAAGTA ACTCCCCGAC CGTCATCTG ACCGTCGATT	TATCTTTGC	360
GACTAAGGTC ACTTTTAAAT CTTGTTCAAA AAATTCGACC ATTACTTGGC	GACAAGCACC	420
ACATGGTGAATC CGGTTTTT CAGTTGACC ATAGACAATC AATTCTGAAA	ATTCTCTTG	480
GCCTTCAGAT ATAGCCTTAA AAATAGCTGT TCTCTCACCG CAATTGGTCC	AAAGGATAGC	540
TAGCATTTC GATATTCACT CCCGTGTTAA ACATTTCCGT CTTTGGCTAC	AAAAACTGCT	600
CCGATAGGAA AGTGAGAATA GGGGACATAG GCATGTT		637

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 940 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CTGAGGATAA	TGACATCTGC	CANAGGAGCA	AAACTAGCAA	AATCATCNGT	TGCACGGTCA	60
ATCATGCCCTT	CTTCAAGGC	GATATCTCTC	GAAGCTTGAC	TACGGATTAT	AACCTAAAAT	120
TTCATAATCT	GGATGATCGC	GTTTGATACC	AAGTGCCATA	GAGGCTCCAA	TCAACCCAAG	180
ACCTGCGATA	TAGATTGTTT	TTGCCATAGG	AACTCCTTAA	TAGTCTTTG	TATAGTCTCG	240
GTGTTGGCT	ACCGCTTCTT	TTAGTTCCTC	AAGATTATCT	GATGAGAATT	TTTCGAGGAT	300
TTCTTGCGCC	AGAACCGTTG	CTACAACTGC	TTCCATGACC	ATTCCCTGCAG	CTGGAAGAGC	360
AGTCGGATCA	CTTCTCTCCA	CGGTTGCCTT	GTAAGGTTCG	TGGGTTTCGA	TATCCACACT	420
CATAAGAGGT	TTATAAAAGAG	TAGGAATGGG	TTTCATGACC	CCACGAACAA	CGATGGGTTG	480
CCCATTAGTC	ATACCACCTT	AAAAACCAACC	TAGATTATTG	GTACGGCGAG	TATAACCGTC	540
TTCTTTAGAC	CAGAGAATT	CATCCATAAC	TTGGCTGCCT	TTACGATAAC	CAGCCTCAAA	600
GCCAAGACCA	AATTCCACCC	CTTTAAAGGC	ATTGATAGAG	ACAACAGCTT	GAGCCAATCT	660
TGCATCCAAT	TTTCTATCCC	ATTGGGACAT	AGGAACCAAG	ACCAACTGGG	AACGCCTCCG	720
ACGACTGTCT	CCACAACCCC	ACCGATGGTA	TCACCACATCAC	GTTTGATTG	GTCAATATAG	780
TCCTTGATTT	CCTGTTCTCG	TTCTTGGTTG	ACAATAGAAA	ACTTCAGAC	TGGGCAGCTC	840
TTTGCTTAA	TTTCAGCGA	CTGTCAGATT	TTCCAGGAAC	ATCCATTCCC	TTGCCACCAA	900
AGACCACGAC	ATGGTTGGCA	ATCTCCATAT	CCAGATTGCA			940

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 990 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GATTCTACAG	GATCCATTTC	ACTATCTTAC	GCGCCGGAA	GTAGGCTGAG	ACATAACCAA	60
GTAATAGAGC	CAACAACTAG	AGTTCCCTAA	ACAGATAAAA	GATTTAATTG	AAAAACCTTA	120
GTGATGGATG	GGTAAAAGTG	ACTTACAATC	GCATTCGCCA	AACTTCCCAC	CCCTTGTGCA	180
ACCAAAAATG	CCAGCAGCAA	GGCGATGCC	ACAATCCAGA	TAGCCTCGTA	AATAAAAATT	240
CCTTGACAT	CACGATTCTG	ATAACCAACT	GCTTTCATGA	CACCTATTTC	CTTGGAACGT	300
TGCATGATAT	TGATGAAAT	AATGATACCA	ATCATAACCG	CTGCTACCAAC	AATAGCTTGT	360

GATGAAAGCA CAATCAATAA TCCCTGAATA ACACGAATAA AGGTAATCAC AATATCAAGA	420
ACTCTCTGTT AAGAAAGCAC AGTATACTTC TTATTTTCT GTATTCTTC TGTTACTACT	480
TTTGTCTGTG ATGGATCTTT GAGTTCCAAG ATAAAATAAG ATACAGCTTT CGTAAATCCA	540
GCCTCTTCA AAATCGTTTC CATTGATGA GACAGCATGA AACTGTTGCT GTCCTCCATG	600
TCATCTTCAT CATTGATTAC ACGTACAATC TTCGTTGAA ATTGAGCAAT CTTACTAGTT	660
TCGGCAGCAC TTTCTACAAT GCTGACTGAG ACTGATTGTC CAATAAGATC ATTAGCTGTC	720
AAATTTTTC CTGTCTGTTC ATTCCAATT TTTAGTAAAG CTGCTTGAA TCGTTAATCC	780
CTGTTCATTT GTATCAGTAT AGAGGGATCC AGCCAACACT TTGTCGTCT CATTATTACT	840
AACAGAGATA CTTGTATCAT CATAAAGACT CACTACTTGA GCATAAGAAG CATCGTTGA	900
CTCAAATCCA TTTCTTGCCC ATCTTTCTT GCCCATCTAT AGTAATATTT GACATGTTCA	960
TCCCNAAGG ACTCTCCAAA TATNNNATAG	990

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ATCGGCTAAG ATGCGTGGAG CATCACAAAT TATCCTTATG AGCCGTCATG AAGACGTCAA	60
AAGATGGCTA TGGAGTCAGG TCGCACAGCT GTTGTGAG AACGTGGTCA AGAACGAATT	120
ACCAAGGTGC GTGAAATCCT CGCGCGGAGGA GCAGACGCAG CACTTGAATG TGTTGGTACG	180
GAGGCTGCTA TAGAACAGGC GCTAGGTGTT CTTCATAATG GAGGGCGTAT GGGCTTTGTA	240
GGAGTCCCAC ACTATAATAA TCGTGTCTT GGTCGACAT TTATGCAAAA TATCTCTGTA	300
GCAGGTGGGG CAGCTTCTGC TACAACATAC GATAAGCAAT TTTTACTAAA AGCCGTCCCTT	360
GATGGTGATA TCAATCCAGG TCGCGTCTT ACTTCAAGTT ATAAACTGGA AGATATCGAC	420
CAAGCCTACA AAGATATGGA TGAACGTAAG ACCATTAAGT CTATGATTGT AATCGAATAA	480
AAAACGAATA GGAGTTTAG AACTCTATTC GTTTTTATG TTATCCTATT CTTGATTTAA	540
GGTACTTTCT CTTAATGTCA GTCTGGTCC CAGCATGGTC AGGCTAGGGA TTTTCCGACC	600
GTGGAGGACT TCCTTGTAA GAATATCCAT ACCTGCTCGG CCCATTTCTT CAGTATAAAC	660
TGTAATACTA AGAGAGGGGA GGATAGACCT GTTTGGTCAG ACTAAGTGTGTC GTTAAAAGGA	720
AAATGAGGCT GACCGGATCT GGCAGGCTGA TTCCAGCTTC TTGGAGGGCA CGGAGGGCAC	780
CGATAGCTAA ACTATCGCTG GCTCGAAAA ATGCTGGCGG AAGTTGGTCT CCCAAGCTCT	840
GAATGGCCTC CTTCATTAAG TCATAGCCAG ACTGGCAGT AAATCTTCCT TGAAAGACCA	900
GTTCATCATG ATAGATTCCC CTCGCTTGAC TGTAGTTTT GAAGTTTCT AGACGCTTGT	960
CCTGAATGAT TTCTTCTTGG TCTGTAGTTT CTTCAAGGCC TGTTAGAATC CCGATAACGGT	1020
CCATTCCCTG ACTGAGGAAA TAATCGACAA CCTGTTCAT AGCAGTGTAA AAATCCGTGA	1080
TAATACAGGT ATGTCCCAGG GAAAGTGTAT CGCTGTCTAG AAATACAAGA GGCTTTGGT	1140
ATTCTTCAAAGG GGCAGAAATC TGAGCTTCTT GATAGGATTG ATTCTGCTAG GGATAACAGC	1200

CAAAGGCAAT CCTCCCTTTA TCCACCTCAT ATTTGAAACC ATTCAGCTC TTA

1253

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CGTGTACCAT CAAGAGGCTA ATTGATGTTT CTTCCCCCTG TGCCCTCTTT GTCAACATTT	60
CTGTTTGAGC CTTATGCGCC TGTAAATAAGG CAGCATTGCG ATCAGCTAAT CTTCGATTGG	120
CTTAGAGAAA ATCCCCTTTT TTTGCTGCCCT GAATAGCCTC CATAGCATTAA CTTTTGGCTT	180
CCCCACCATA CATAATTAGC CCCATTACAG ATTCTAAATT ACTTTCATCC ATAACATTCT	240
CCTCAATCTT AGTCTAATAA ACTTTCAGCT AAATCTAAGA CTTTGAACC ATTCACTCATT	300
CCATAATCTG TCATCGGAAT AACCGCCACA GGAATCTGTC TATCTTTAG TTTTCTTGA	360
AAGTCCCCTA GTAAATAGCG AACTTGAGGA CCTAAAAGCA ACACATTAC TTCTTTGTT	420
GCTACAATTCTT CTTCTGCTTC AGGAGCTGGA ACTGCAAAAA TTTCTGCATC CAACCCCTTA	480
TCTTCTGCTG CTTTTGCACT CTTTGTCACT AGCAGACTTG TACTCATACC TGCTGCACAT	540
GCTAACATAA TTGTTACTTT AGCCATAGCT TACTCCTTTA TCACCTATTT ACTGACCTAG	600
CCAAGCGAGA TACTGTATGT CTCACTCCTC TAATTGCCTT GCTCAATGCA TAAATATTAT	660
CGACTGTTGC CAGTCCCCCA TATCCTGCGT CACCTATATG TTGAATATCA ACTCCACAAA	720
TTTTATTCTT AAGTGAATT CCCTTAATAG TATCTGTATC AGATGTTCT TGGCTAGTAC	780
CAATAGCACT CAATACAAGA CCACCCCTAC TATGAACGAG ATCAACGACT TCACGCAACT	840
CTTGGTCATG AAAGGCTGGA ACGGTTCCAA CTGCTGGAAC AAGTATCACA TCCGCACCTG	900
CTTCCAACAA TTGCTCTGCG ACAGAAAGCT CTGCCACAGG CTCATTCACT CCTGCCCGT	960
GCATCTTACC TGCAATAATC AAACCAGAAA AGTTTCCCTT AGCAGTTGA ACAGCCTTAA	1020
TGATTTCTCG ATTGCTAACT CCTGTTCCAG GATTCCAGT CAAACAGACA AAGTCAAAAC	1080
CTAACTCCTA TATTCGCTTC AATGTTCAA CACTAGCAAC ACGACCTGCA ACAATTTCCT	1140
GTGTTTCCTC TAGCATTCTT TGCAGATGGG TCAATCGGTT CCAAATTAC ACCAATTGGA	1200
CAAGCAACAA G	1211

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CCACACTAGC AGCCTATGGA CTCACTAAAA GAAAAGAAGA CTAAGTCTTT TCGATAAAAA	60
ATAAACAGCG AGATTGAAGC TCGCTGTTA TTTTTAATT AATCACCTAG TCCAAGACGT	120
TCAAAGATAT CATCCACTCG TTTGGTGTAA TAAACTGGGT TGAAGATTTC ATCGATTCT	180
TCTTGTGTGA GACGTGATGT TACTTCTGAA TCTGCCTCAA GAAGTGGTTT AAAGTCTACT	240
TGGTTGTCCTT AAGAGTAGGC TGTTTTGGT TGCAACAGT CATAGGCTTG CTCACGGTC	300
ATGCCTTTT CAATCAATGT CAACATAGCC CGTTGGCTAA AGATAAGACC AAAAGTCGAG	360
TTCATGTTTC GGATCATATT TTCTGGGAAG ACTGTCAAGT TCTTGACGAT ATTTCCAAAA	420
CGGTTGAGCA TGTAGTCAT CAAAATGGTC GTATCTGGTG TGATGATACG CTCAGCTGAT	480
GAGTGAGAAA TATCGCGTTC GTGCCAGAGA GCGACGTTT CATAAGCCGT AATCATGTGA	540
CCACGAATGA CACCGGCCAG ACCAGTCATA TTTTCAGAAC CGATTGGGTT GCGTTGCTGA	600
GGCATTGCTG AAGACCCATT TTGCCCTTA GCAAAGAACT CTTCTACTTC GCGTTGCTCA	660
GATTTTGTA GACCACGAAT CTCAGTCGCC ATACGTTCGA TTGAAGTCGC AATGCTGGCA	720
AGAACCGCAA AGTACTCAGC GTGAAGGTCA CGAGGAAGGA CTTGTGTTAA AGATTCTTG	780
GGCACGGATG CCAAGTTTAT CGCAGACATA CTCCTCTACA AATGGTGGGA TATTGGCAAA	840
GTTCCCAACC GCACCAGAAA TCTTACCAAGC TTCTACACCA GCAGCCGCAT GCTCGAAGCG	900
CTCCGATATT GCGTTTCATT TCGCTGTACC AAGTTGCTAA TTTAAGGACC AAAGGTTGTC	960
GGCTCAGCGT GCACACCATG AGTTACGCC CATCATGATG GTGAACCTGT GCTCCTTGGC	1020
TTGTCAGCGA TGATATTAGT GAAGTTTCA AGGTACCGAC GGATGATGTC GTTGGCCTGC	1080
TTGTAGAGGT AACCATAAGC AGTATCCACC ACGTCGGTAG AAGTTAACCC ATAGTGAACC	1140
CACTTGCCT CTTCACCAAG AGTCTCAGAA ACCGCACGCG TGAAAGCCAC CACATCGTGG	1200
CGCGTCTCCT GCTCAATTTC CAAAATACGG TCGATGTCAA AGTCCGCCTT CTTGCGAATC	1260
AAAGCCACAT CTTCCCTTAGG GATTTCCCCA ACTCAGCCA TGCCCTCGTCA GAGAGGATT	1320
CCACCTCAAG CCAAGCACGG TATTTATTTT CTTCACTCCA AATATTGCC ATCTCAGGGC	1380
GAGAGTAACG GTTGATCATG TGTAAATTTC TCCTTCTTC TTAAG	1425

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CTATTCTGAG TATAAAGTTG GCGGAGGCTG GAACTACGCT CGTTATGAGG TCATAAACTA	60
CTATACTGGA GGTTATTAAT CCTTAAAGAG TGAGAAAAGG AGGGCTGGAT ATGTTAAATC	120
TTACTCATGT TACCTTAAAA ACGCGACAAG TCATCTTGCA AGATGCGGAT TTTACCTTTA	180

AAAAGGGTAG GATTTATGGC CTTCTTGCTA TCAATGGCTC GGGAAAGACG ACACTATTCC	240
GAGCTATGAG CAAGTTGCTT CCCCTTAGTA GTGGACACAT CGCAGTTCCT CCTTCTTGT	300
TTTATTATGA GAGCGTTGAA TGGCTGGATG GAAACTTAAG TGGGATGGAC TACCTTCGTC	360
TCATAAAAAA ACATCTGGAA GTCAGACCTA AACTTGAGAG ATGAAATCGC CTACTGGAA	420
ATGGCTGACT ATATCAGTCT TCCCATCCGC AAGTATTCCCT TAGGGATGAA GCAACGTTG	480
GTGATTGCTA TGTATTTCT CAGTCAGGCC AAATGCTGGC TCATGGATGA GATTACAAAT	540
GGCTTAGACG AGTATTATAG ACAGAAAGTTT TTGATAGGC TAGCACAAAT CGATAGACAA	600
GAACAGCTGG TTCTTTAAG TTCCCACAT AAGGAAGAGT TGGTTGATAT CTGCGATAGA	660
GTAGTAACCA TTCATCAGGG GCAGATAGAA GAGGTTAGT TTATGAAAGA TGTTAGTCTA	720
TTTTTATTGA AAAAAGTTT CAAAAGTCGT TTAAACTGGA TTATCTTACT TTTATTTGCA	780
TCTGTACTCG GTGTTACCTT TTATTTAAAT AGTCAGACTG CAAACTCAGT CAGCTGGAG	840
AGAGAGTGG AAACTCGTCT TGTAGACCGT GAGAGAGTCA TCAATGAAAA TGAAGAGAAA	900
CTCTCCAAA TGCTGATAC CAGCTCGGAG GAATACCAGT TTGCTAAAAA TAATTTAGAC	960
GTGCAAAAAA ATCTTTGAC GCGAAAGACA GAAATTCTGA CTTTATTAAA AGAAGGGCGC	1020
TGGAAAGAGG CCTACTATCT GCAGTGGCAA GATGAAGAGA AGAATTATGA ATTTGTATCA	1080
AATGACCCGA CTGCTAGCTC TGGCTTAAAAA ATGGGGTTG ACCG	1124

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1089 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

CAGAGCAACT TCGTCAAATC TTCATAGGTG AGGTAACCAA TTGGAAAGAG GTTGGTGGTA	60
AGGACTNACC CATCTCTGTT ATCAATCGGG CAGCCGGCTC TGGCTCTCGT GCTACCTTG	120
ATACTGTCAT TATGGAAGGT CAGTCTGCCA TGCAAAGTCA GGAGCAGGAT TCAAATGGAG	180
CGGTAAAATC AATCGTATCA AACAAAGTCCA GGAGCTATCT CTTATTTATC TCTTACCTAT	240
ATAGATGATT CGGTCAAAAG CATGAAGTTG AATGGCTATG ACTTAAGTCC AGAAAATATA	300
AGTAGCAATA ATTGACCCCTT GTGGTCTTAT GAGCATATGT ATACATTGGG GCAGCCCAAT	360
GAGTTGGCTG CAGAATTCT CAATTTGTT CTCTCGGATG AGACCCAAGA AGGGATTGTC	420
AAAGGATTGA AGTATATTCC GATTAAGGAA ATGAAGGTTG AAAAAGATGC TGCCGGAACT	480
GTGACAGTGT TGGAAGGGAG ACAATAATGA ATCAAGAAGA ATTAGCTAAG AAAATGTTGC	540
TTCCATCAAA GAATTCTCGT CTGGAGAAAT TAGGAAAAGG TTTGACCTTT GCCTGTCTTT	600
CTTTGATAGT CATCCTTGTG GCCATGATT TGGTTTCGT AGCGAAAAAA GGCTTGTCGA	660
CCTTCTTGT CAATGGTGTG AATATCTTGT ACTTTCTTTT GGGAGGAAC TGGAAATCCTT	720
CTAGTAAAGA ATTTGGTGCC CTTCCTATGA TTTTGGGTTG CTTTATCGTT ACCATTCTCT	780
CAGCCCTTAT CGCAACACCC TTTGCTATTG GTGCAGCAGT TTTTATGACC GAAGTATCAC	840
AAAAGGGGC GAAGATTTG CAACCAGCTA TTGAACCTCCT GGTTGGGATT CCTTCAGTAG	900

TGTACGGATT TATTGGCTTG CAAGTCGTCG TTCCCTTGT TCGCAGTGTC TTTGGTGGGA	960
CTGGTTTGG GATTTGTCA GGGATTCCG TCCTCTTGT CATGATTTG CCGACCGTAA	1020
CCTTATGAC AACGGATAGC TTGCGTGC GG TTCCTCCNTT ATTATCGTGA AGCCAGTTTC	1080
GCTATGGGA	1089

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1502 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CTNTNTTAA ACCTTGACCT TANTTGANNA TTATACCGAA ATTNTCTTCA TTTTTAAAAG	60
AAAAAAAGGGC GCTGGTAAAA GGGATAATCT TCACCAACTC CCTATNTTTC TACTTATCTA	120
AGCCTAATTC TGCCAAGATT TGACGTTGT NGGCAATCTT TNGGACTTCN TNGTCTCAT	180
CTTCAGACCA GTCTAGTTA ATTTCTGAAA CAATCTGCC AGGGNGATTT NTCAAGATAT	240
AGATGCGGTC GCTGAGANTG AGGGCCTCCT CAATACTATG CGTGANGATC AGGGTTGTTA	300
GCTGCAACTG CTTGTGAATC TCAAGATACC AAGCGTGGAG TTCCATCTTT GTCATCTCAT	360
CCAAGGCCT AAAGGCCTCA TCTAAGAGAA AGAGCTTGTG CCCAAAAAGG TAGGTCCGGA	420
GTAAGGCTAC ACGCTGGCGC ATCCCACCGC TAAGTTCATG AGGATACTTG TCTCTTACAG	480
CTGTCAGCTG GAAGGTCGCA AGAATTTTAT CCGCTCGGGA AATAGCTTCT GCCTTATCCA	540
CCTTTGAAT CAAGAGGGC AGAATGATAT TTCCAAGCAC CGTCTTGTGC TCCAAGAGCA	600
GATCCTTTG CAACATATAA CTCACGTGCC CCTTGGGATT TTCTTCACCA TCAAGGACAA	660
TTCTCCCTGA CTGAACCTCT AAAATCCCAG CGATTAGATT AAAGAGGGTG GTCTTCCAA	720
CACCACTTGG CCCTAGGATG GAAACCACTT CGCCTGAAGT CACCTGTAGG TTGATATCCT	780
CTAAAATCCT CTCCGTACCA TAGGCATAAC TGACGTGCTC TAGTCTAATT TCTGTCATTA	840
TTTCACAAAT TCGTGGTGA AGCCTTGTC TGTCAAGTCT TCTTAAGGA TACCATTTC	900
TTTATCCCAT TTATAGAAAG CATTCCAGCG AGCTGCGTCA AATTGACCCC ATTTTCCCT	960
GTCGCTTGGC TATTCTTTG ACAAGTATTT TTGAGATTG ATGACAAAGT CACGTTTTC	1020
CTTGAGTTCA GGTGCATTCT TGATGAGAAT ATCTGCAGCT TCTNCTGGAT GTTCCATGGC	1080
ATATTGGTAG CCTTTNTGA TGGCTTGGAT GACTTGCAGA GCTTCTTCTT TGTTATCTT	1140
CAGATAGTCG TTGTTGCAGA TGATAACTGG TGAATATTAN TCAAACCTCT TGACATAGTC	1200
TTTCAAANTAC ATGAAGTTAG CATCTACACC TTGAGATTAA GCAAGGATAC CATCCCAACC	1260
GTAGTAAATC CNAGCACTAT CAAAGACGCC ATTGGCAATC GGTGTGATTG AGTTTGAGTC	1320
NTTANTTGGT ACTNTTCAA CCTTCTCACA GTCTCCNCCT TGAGATTCTA CCAAGGTTTT	1380
CAACATACNN GTTCANTTGG GTCATTCCAT GTCCCATATT TCTTACCAAC CAAGTCTTTT	1440
GGACTGCCTA CATTNTCACA TTACCGAGAG ATGATCCCTG ATGTATTGTG TTCCACCNAT	1500
AG	1502

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1022 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ACTCTTCAGC GATTCTTGG CTGAGAATGT CCTCATAGGC AGGGAGTTGG ATGTCCTGAC	60
CATATTTCTT CTTGAGGGCA GTAGTAAC TA GGCGATAAGC CAGATTGGCA TTACGAGAGA	120
AGATAGGCCCG GNNGAAANTAC GAACCAAAGA CATTCTTATA ATGAACCCCT TCACCGACCT	180
TTTCTTCGTT GTTTCCATT CCATAGACAA CCTGTCCCAG CGGTTTTGG TCATCAGAGA	240
GGAAGGTACG ACCTTGGTGA TTTTCAAATC CATACTAGGT TTCATCGAAA TCTTTCATTG	300
TGAATCTTGA TGTCACCGAT AAAACGGTTA TTGGTCTGGT TGAGCGTGTGTA GTGTCCCAG	360
ACCCCTAGCC CTTCGATACG TTTTCCCTGAA GCTTCAACAT AATATTGACC CAATAGTTGG	420
AAACCACCGC AGATAGCCAG AACTACACCG TCGTTTTGGA TGTAGTTGTC AATGCTCTCT	480
TTTTTAGCAG GTAGGTCGTC TGCAATGATA CTTTGTCAA AGTCTTGACC ACCACCGAAA	540
AAGGCGATGT CGTAGTGATT TTCATCAAAG TCATCATGGA GAGAAACGAT GTCAACGGTC	600
ACATGGGTTCC CAGTTTTTC AGCCACATAC TTGAGCATGA GGATGTTCC ATTGTCCCCG	660
TAGGTATTCA TGAGATTTCG GTAGAGGTGG GCAATGTTGA GCTGATAGGG GTAATTGCCA	720
TCTTTGAGG AAAGTGAAGT ATAAACCATT AGTCATCTC CTTTCTAACCA ATCTGACGAC	780
TAGCCAGCAG TTCACGAAAT TCCAGCATGG CAGTATAAGT TGCCAGAATA TAGGCATGCT	840
TGCACTCTTG ATTCTCAATG GTCTTGAGAA CTTGCTCCAG ATTACTCGTT TCAGTGATT	900
TCTCAGCTGG ATAGCCAGTC ACTCGGAGGC GACCGAGCGAT TTCAGAATGA CGAACACCCGC	960
CAGCGTTGAT TTCAGGAATG TCCATGTCAG TGATTGCTC AAAGTCTGCA TCCCAGATCC	1020
AG	1022

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CCTCCAGGTC TCGGGAAACG ACCATGGCCT TTGTTATTGC CAACGAAC TG GGAGTCAATC	60
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TTAACGAGAC	GTCGGGTCCA	GTCATTGAAA	AAGCCGGAGA	TCTGGTAGCT	ATTTTGAATG	120
AGTTAGATCC	TGGGGATGTA	CTTTTATTG	ATGAGATCCA	TCGTTTGCCA	ATGTCAGTGG	180
AAGAGGTGCT	TTATAGTGCT	ATGGAGGACT	TCTACATAGA	TATTATGATT	GGGGCTGGTG	240
AGGGTAGTCG	TAGTGTCAT	TTGGAGTTAC	CACCTTTAC	CTTGATTGGT	GCGACGACTC	300
GGGCTGGTAT	GCTCTCCAAT	CCGCTACGGG	CACGTTTGG	GATTACAGGC	CATATGGAGT	360
ATTATGCCCA	TGCTGACTTG	ACAGAAATTG	TCGAGCGGAC	GGCAGATATT	TTTGAGATGG	420
AAATCACTCA	TGAGGCAGCA	TCTGAGTTGG	CCCTACGTAG	TCGTGGGACC	CCTCGTATTG	480
CCAATCGTCT	CCTCAAGCGC	GTGCGCGATT	TTGCCCAGAT	AATGGGAAAT	GGGGTAATTG	540
ATGATATTAT	TACCGATAAG	GCTTTGACTA	TGCTGGATGT	TGACCATGAA	GGTTTGGACT	600
ATGTGGATCA	AAAAATCCTT	CGTACCATGA	TTGAGATGTA	CAGTGGAGGA	CCTGTTGGTC	660
TAGGAACCTCT	TTCTGTTGAA	TATGCCGAA	GAACGTGAGA	CAGTGAAGA	TATGTATGAG	720
CCTTACTTTG	ATTCAAAAAG	GTTTTATCCA	TGCGGACACC	GTCCTGGACG	GGTGGCGACT	780
GCCTAAGGCA	TATGAGCACT	TAGGTTATGA	ATACAGTGAA	AAATAAGCAA	GAAATCCTTA	840
GAGGCTTTT	AGAGAAAATC	CAGATATGAT	GGCCATTCTG	ACGATCATCC	GAGACCTTGG	900
TCTGAAAGAC	TCGTGGTTGG	CAGCAGGTTTC	TGTCAGAAAT	TTCATTGGA	ATCTTTGTC	960
AGACAAATCC	CCTTTGATC	ATGAAACAGA	TATAGATGTT	GATTTCTTT	GATCCCAGAT	1020
TTTCTTATG	AGGAAACCTT	ATTACTGGAG	AAAAAGCTGT	GAGAGGATTT	TCCTCAGTAC	1080
CAGTGGGAAT	TGAAAAATCA	GGTCTATATG	CATCAGCACA	GTCCTCACAC	TGCTTCCTAT	1140
ACCAGTTCTC	GTGATGCTAT	GAGTAAGTAT	CCAGAACGGT	GTACCGACAGT	TGGACTGCGC	1200
TTGAATGAAAG	AATCAGATT	TGAACTCTAT	GCACCTTATG	GTTTGGAGGA	TATTTGAAAT	1260
TTCAAGTTCG	TCCAACTCCT	CATTTCTTAG	AAAATGAAGA	CCGAATGGAA	CTCTATCAAA	1320
CACGTTTATC	CAAGAAAAAT	TGGCAGGAGA	AAT			1353

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

CTCCTGGAAA	TTCTGGCAAG	TAGGCTGGAT	GAATGTTGAC	AATCCGACCT	TCATAAGCCG	60
ACAATAAGGT	TGGTCCAACG	ATTTTCATGT	AGCCTGCTAG	GCAAACCAAG	TCAATCTGGT	120
GTCTTCCAA	GAGTCGACA	AGGGCTGCTT	CGTAGTCTGT	CTTGCTCTCA	AACTCCTTGA	180
GTCAAAAGC	ATAGGACAGA	ACGCCGAGCT	GCTTTGCACG	CTCAAGCACA	TAGGCATCAC	240
GATGGTCTGA	AAAGACAAAC	TCCACTGGAA	ATTCTTCGGC	AATCACCTGA	AAATTGAGC	300
CATTACCAGA	GGCAAAACC	GCTATTTTT	TCATTTGATA	ATGACACTT	CGTTTTCTTT	360
CTTGACGATG	CGACCAATT	CATAGACTGC	TTCATCCAAC	AATTCTTTA	CACGCTCTAC	420
ATTTTCAGGG	CTGACCGCCA	ACATAAGTCC	CACACCCATA	TTGAAGATT	CAAACATTTC	480
TTCGTGTTA	ATCTGACCAT	ATTTTCAAG	GGCTTGAAA	ATTGGAAGCA	CTGGAACCTT	540

GCTTTCATCA ATTCAGCAG

560

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 860 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CTTCAACACT TTATTTTTAT CTTTCTCCCA TTTCGTATGC TAGTCGGAA ATTGTTGCTA	60
GAACCTCTCC GACTATTGAG GATGTTCTCA TTGCTTTGT AGGAGGGATA GCAGGTATTA	120
TTGGTGCTAG GAAAAAAAGAG ACCAATAATA TTGTTCCCTGG TGTTGCTATT GCAACCGCCT	180
TGATGCCTCC TCTTTGTACA GTAGGTTATG CTATTGCTTC TGCTAATCTA AAATTTATCA	240
TTAGGCTCCT CTTACCTATT CCTCATCAAT TGTAGCTTA TTGTCATTGC GACTTATATA	300
GGTGTAGGT TGATGATGGT TAAGAACAT TATTTAAAG ATAATGAAGA AGACTCTAAA	360
ATGCGTAGGA TTTTGCTTCT AGTTGCTGTT TTGCTGATGA TTCCGAGTTT CATCTCTGCA	420
ACGACTTTAG TGAGAGAAC GTTGAAAAAA GAGTCCCTTA AGAAATTTAT ATCAGAGCAG	480
TTTCAGGGGC ATAATATTTT GAAAAAAACC TATTCTAAAA AGACTCATAAC CCTAAAGCTA	540
ACCATTTCAG GAAATTATTT GACAGAAGAA GAACTCGATA TGATTCAAG TAAGAGAGGT	600
GACTATGGTT TAAGTGATGT TTCTGTCATGTTTACAAT TGTCTGATTC AGAACAACTT	660
AGTAAGGAAG AACTGGTGGA GTATTTCTTC CAGTATATCA AGGATAAGGA AGCAAAAGAA	720
AAGGAAAAAG CTAATAAGTT TTATACAGAG TCTGAGGAGC AATAATTCT TGAGAATAGC	780
TGGTTTTCT CGTGAGTCTT CTATGTATAT CAAAGGAAGA CTGAGGTTTT AAGTATGAAA	840
CTTTTCTTCT ATTATAGTAG	860

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 925 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

TCTGGCCAA CTGCATGGAG TTCAGCGGTC AATTCACCG CACCTGAGAA ACAGACCCCT	60
GCACCCCTGA AATCTCAGGA GACATGATGG TCTGGATGGA ATCAATAATG AGAAAGTCTG	120

GCTGGATACG CTACCACTTC TGCACGAACA CTCTGCATAT TGGTCTCTGC ATAGAGATAA	180
AACTCACTAT CAAAATCACC TAAGCGCTCT GCACGTAGTT TAATCTGCTG GGCAGACTCC	240
TCCCCACTGA CATAGAGAAC TGTCCTTCACT TGGGACAACG GGGTTGAGAC TTGTAGGAGA	300
AGAGTTGATT TCCCAATCCC AGGATCCCCA CCGATGAGGA CGAGACTTTTC CTGGTACAAC	360
TCCGCCTCCA AGCACACGGT TGAATTCCCTC CATCTCCGTC TTGGTTCGAT TGACATTGAT	420
GGAAAGTCACC TCAGCTAGTT TCATGGGCTT GGTTTCTCA CCTGTCAAGG ACACACGCGC	480
ATTCTTGACC TCGGCAACCT CAACCTCTTC CACAAAAGAA GACCAAGAGCC CACAGTTGGG	540
GCAACGTCCC AGATATTTAG GGGAAATTATA CCCACAATTT TGACATACAA ATGTCGCTTT	600
TTTCTTGCG ATGACAAACC TCTTCTATA TCTCTAACTC ACACCTCAATC ACTTGGCAAA	660
AATCAATCTT CTCATTTGGC ACAAACTGGC GCATGAGCAT TCGATGAGCA ACAACTACCA	720
CAGTCTGATG TTCTCGATAC TTAAACATAC ATTCTAGAAA CCGAGACTTC ATTTCCGTAG	780
CTGTCTCATA TTGAATAGGA CTATTAGGAA GCAACTCCCC CTTGTTTCT AAAAACAGTC	840
TTCTAGCTGT TTCAAAGTTT TCTATTCCCTG TTTTATAGAC CTGCCATTCA TGTAATAAAG	900
GCTCTACTCT TAAAGGAAGA CCCGT	925

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

TTCTNGATCA AGTCAAGGAC TGCANGCCAC GACCGACATA GCGTTGGCA ATGGAAACAA	60
CCAAACGAAG ATTGGCTTCC GCAAGACGTT GTTGGCTTC GATATGCCA GCTTCAACAG	120
CCAGTGCCAA CTCTTCTCC TCTTCATTGG TCAAGAGAGG AACGACCCCT ATTTCTTCA	180
AGTACATACG GACAGGGTCA TTGACCTTAG CAGAAGTTGA CCCAATCAAG TCCTCATCGC	240
TGAGTTCTGG TTCTTCTTCA TTGCTAAGAA CACGCGCACT TGGATTTCT TCGTTATCTG	300
TGATAGAAAT GCCTGCATCC TGAATCCGTT GCAAGAGATC TTCAATCCC TCAGCGTCCA	360
AGGTAAAAGG AATAACCAGA CTTGCATTGA TTTCATCATC TGTGCTGTC CCTTTTGCT	420
TATGATTACG GATAAATTCT GCTACCTGTA CGTCAAATGT TGTTACTTCT TTTTGTGTTG	480
TTGCCATTAT TACTCCATTC TTCTCTTTG GGAAATTAAA CGTTCCAATT CTTCTAGGGC	540
TGTATCTGTA TCTCCTACAT GGCTAGCTTC CTGCACCTTC TTTTGATTC CCATATTGTC	600
CTGATTCAAG AGAGCCTTGT TTCGAAGTCA	630

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

CTAGGGCCAT CTTCTCACCT CCTCCTTGT	AGTACATTCT TGCAATAGAA AAAATAAGAT	60
TGAGTCCCCC CAACCTTAAA TTTTTTCA	CC ATCTTCTTT TCTTAGCAA TTTGCTCTT	120
GATTTTCTT TCTTCTTCTT CTTGCGCG	TTTTCTTCTC TCGATACGGC GACGCACTGC	180
TTCACGTTT CCTTCTGGAT CTGGGTGAAT	TGTAACGTTT CCTGATTGAA TTTCTTCTAA	240
AGCGCGAAGA GTTGATTTT CAGACTGAA	ACCTTGAGTT GCTGGGCAC CTGCTTCCAA	300
TTCGTGGCA CGTTTGCTT CCAAGATTAC	GAGTGAATAT TTTGAAGGAA CCTTGTGAG	360
CAAGGTATCA ATAGAGGGTT TTAACATCAT	TTGCTTGTAC CTATTTCTA AATTTTATCG	420
GGTAGTTGGA GATTGGTA ACATCTCCTG	ATAGTGACCA ATGACACGAT CCACACAGAA	480
GTGTTCTGCT TCAATCACAC ATTTGACACG	TTCAGCAGCT AGGGGTACCT GATCGTTGAC	540
AATCGCATAA TCATACTCAC GCATGAGGGC	AATTTCTTCC TTGGCCTTTT CGATTGTTG	600
GGCAATCACT TCTGCACTAT CTGTTCCACG	ACCTACCAAG CGTTCTTGCA ATTCACTCAA	660
ATCTGGTGGT GTCAGGAAGA TAAAGACAGC	ATCTGGAACC TTTTCTTGA CCTGAAGAGC	720
ACCCCTGAAC TCAATTCAA GGAAAACATC	GATTCCCTTG TCCAAGGTTT CATTGACATA	780
GGTCAGAGGA GTTCCATAGT AGTTGCCGAC	ATATTCTGCG TATTCCAACA TCTGTCTTG	840
ACGAATCAG		849

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 581 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GCCAAACAAAC GCATCCATAA TGGTTAAC	TC TGATAAGGC AGAGCTACAT TCAAAACAGC	60
TTGCTGGTTT GTAGGCTTTC AATCAGAGCA	ATCACTTCTT CAACCTTGT	120
GCAGCTGTCT CAATCTTGT	AGC ATCAAGA	180
TTTGACTTGG TACGGCTAGC	AA TCTGAAATG	240
TTTGAAATAG CAACTGGC AACGCC	CAACCAATAA	300
TTCCTTCCTC TTCTTCTAA	CTAGTAAACG ACTCATTTT	360
GTAAGTTGC AGTGTAGTAT	TCTGTGAAA GCTGGCGTT	420
AATCTTGAC AGGGTGGTAT	TTTTCTGATG CAAATCCAAA	480
TAGTTGGAAT ATGGGCCTGA	CAACCAATAG CCAGCTGGC	540

GCATGCTTCG GCAGGCCGAC TCATCCTCGT CAAAGAAAGG A

581

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

TTCTGAAAAT CCATACTTCT ACCAAGGAGA TACGCTAGCG GTCTCGGAAG TTCTCATACT	60
TCTATCGCTA TATCTGGCCA TCGCCTTTCT ATCCAAGGAT TGACAACAAG AGATAAGGCA	120
GAGAAAAAAAT TCTTGCTGGA TCAGCTGGTT GCCTGCGATG GTGGTACAGG TGTCATGCAC	180
GAAAGCTTCC ATGTAGATGA TCCGACCCTC TACTCTCGTG AATGGTTCTC CTGGGCTAAC	240
ATGATGTTCT GTGAGTTGGT CTTGGATTAC TTGGATATTG GCTAAGGGGC TCGCTTTAGC	300
TCAACCGATT CTTATCAGAA TCACAAGTTT ACATTTAAAA CGTTAAAATT TAAATTAGA	360
ATGAGGTTTT ACTTCATGGA AAATGTTGTT GTACATATTA TCTCACATAG CCACTGGGAT	420
CGTGAGTGGT ACTTGCCTT TGAAAGCCAT CGTATGCAAT TGGTGGATT GTTGACAAT	480
CTCTTGATC TCTTGAAAAA TGACCTGAG TTCAGAGTT TCCACTTGGA TGGACAAACT	540
ATTGTCCTTG ACGACTAATC TACAAATTG CCCTGAAAAT CGCGACAAGG TCCAACGCTA	600
CATTGACGAG GGCAAGCTTA AAATTGGTCC CTTTACATC TTGCAGGATG ATTATTGAT	660
CTCCAGTGA GCAAATGTCC GCAATACCTT GATTGGTCAA CAAGAAGCTG CCAAATGGGG	720
TAAATCAACC CAGATTGGCT ACTTTCCAGA TACCTTTGGA AATATGGGAC AAGCGCCTCA	780
AATTCTTCAA AAATCAGGCA TTCACGTGGC GCCCTTTGGT CGTGGTGTGA AGCCGATTGG	840
ATTTGACAAC CAAAGTCTTG AAGATGAGCA GTTTACGTCT CAGTTTCAG AAATGTAUTG	900
GCAGGGTGTG GATGGTAGTC GTGTTTAGG TATTCTCTT GCCAACTGGT ACAGTAACGG	960
GAATGAAATT CCAGTTGACA AAGATGAGGC CTTGACCTTC TGGAAACAAA AATTGTCAGA	1020
TGTGCGTTGC CTACCGCTTCG ACCAACCAAT GTTGATGAT GAAACGGCTG TGAACACCAG	1080
CCTGTCCCCAA AAAAATCTG AGCGAAGCCA TTCCGTGTGG CAAATGAACT CTTCCGGAT	1140
GTAATCTTG TTCATAGTTC TTTGATGAA TATGTTCAAG	1180

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

CTCAAAAAGT	CTGAAATTGG	ATCATTTGGA	ACCATCTGAG	CAGTAAGTTT	AACACCTTT	60
TCTGCCAGTT	TGTGGAAGTC	TTCCACATCC	TTGTCTACTA	CGTTGATAGA	ACGTGTAATA	120
GAACGAGTTT	CTGGTGTGG	AGACATATTC	CCAACATTAA	GGGTTCAAG	TGGTACACCT	180
GCTTCTACCA	AACCAAGGGA	AGCGGTCTGG	TTTACGAGCC	ACGATAAAAGA	GACGTTGGCT	240
ATCGTATTG	CCAGCAAGAA	TATTGGCTGC	AGCTTTCTCA	ACTGGCAAAA	TACTCAATT	300
CACACCTGGT	GGTGTGCAA	GTTTCAAACC	ACTCTTTCA	ATATCGTTGT	TGACAACCTC	360
GTCGTCTACA	ACCATAATGC	GTGAAACATT	TAGTTTCCA	GCCCAAAGAT	TGGCTACTTG	420
TCCGTGGATC	AAACGTCCAT	CAATACGGCA	TCCTACAATT	GTCATAAGTT	TTCCCCCTTT	480
ATATGTTTTA	GTGTAGGTTT	ACGAGTTAAA	TGAATCTCTT	CTTTATATTG	ACCTTCTGTT	540
TCAAAGATAA	TGATGCGGTT	GGCACCTTCC	TTGAGATAG			579

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 736 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

CGCATANCCT	AAAAGTTTC	TTTGACATCT	TCTGGAATAT	CTGTATCATT	AGCTTCCTGA	60
ACATCTCTAC	CATAAATCCC	AAAGGCTGGA	ATCCCTTTT	GAGCAGTGTGA	AGCTAGTACA	120
GCTGCAAGAT	AGACAGCTCC	TGGGCGTTCT	GTCCCATTAA	ATCCCCAAAT	AGCATGAGGA	180
ATATCTGGAG	ACATATCCAT	AGTTTCACTA	CCATAAACACC	AGCATGGTGT	AACTGTAATT	240
GTGCGCAAA	CATTGATT	TTTAAACAAAC	TCATGGGAAG	CTGCAGCCTC	TGGAACACGA	300
CCAATGGTAG	ATGGAGAAAT	CACACATTCC	ACAGGTTCCC	CATCTGGATA	TTTCAATGTG	360
CTTGAAATCA	AATCTGCCAC	ACTTTAGCC	ATGTTCATLG	TTTGTACTTC	AAAGTGAATTG	420
CGTACACCTT	GACGACGACC	ATCAATAGTC	GGACGAATCC	CAATACGTGG	ATGTTGAATC	480
ATACTATTTT	CCTCTTATTT	TTCTGTTCT	TTCATACTAC	CATCGCCATT	ATATTACGG	540
TAGCCTGGGT	GACGACCTGT	AACCTTATAA	TTTCTCGCA	TTGAGAATAG	ACGTTCTAAA	600
GTCGGACGAG	CAATTCTTG	CTCCTCAATG	CCCTTGTAG	AAAGTAACAT	TCTTCCGTGG	660
AAGGTTGTCT	TTGCGACTAA	TTCTAAAGTT	TCCATACGGT	AGTATGCTGT	AATTACATCG	720
CTTCCGACAG	TCAGAG					736

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CTCATTGTAT TTAGGAGAAA TGATGGTATC TTCCAAATCA AAATCAACTT CACTCCATAG	60
TCTCAACGGA TTGATTTCC CATCTTGATA GGTCACATCC TTGTCAAGGA TAAACTGAGT	120
CAACGCCTCA TGCTGACCTT GACACCTGAT GTCATCTACC AAGAGCCAGA CATCCTCTAC	180
CAACATGAGG ATTTTCTCT TGTGAAGATA AGGCAAATCA GGTCTGCTG ACCAATAAGC	240
CCCTTCAATA TAATGCATTC CCTCCCTTTC TTTATGGTGA CAAAACAGGG AGTGAGGATA	300
GTATTCATAT TCCCAGGATC CCGTGATTCT TTCCGGAGCT TTCCCATCTA CAATGCAGGT	360
CGAATGACTC CAAGCACTCT TTAAGAGATA ACGTTCATAT ATCTCCGAT AAGAATAACG	420
CCCAGCATCT ATGAAAATAG GTTGGCCTTG ATACTGTAAG CAAAAACTAT TCTCGTCACT	480
ATGGCTATGG GCACTTCCTA GCGGACCATT TTTGAAAAAT AGATAACGAT GTTCATCCTT	540
AATGCAGACA TGTCCAGAGT CTTCAAAGAT CATGGACTTA GGCTGCCAAG	590

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CTAGTGTAGC TTCCCTTAATC TTATCTGATA AGATAGCTGT CATATCAGAC TCAATCATT	60
CCTGGAGCAA TCACATTGAC TCGTATATTG CGACTAGCGA CCTCGCGTGC CACAGACTTG	120
GTAAAGCCAA TCAAGCCAGC CTTAGAAGCA GCATAGTTAG CTTGACCAAT ATTCCCCATC	180
AAACCAACAA CACTAGACAT ATTAATGATA GCACCTTCTC TGGCTTCAA TCATCGGTTT	240
CCAAAGACTG ATTGTGTAT ATTAAAGGCA CCAGTCAGAT TGACCTTGAG CACTTTTCA	300
AAATCTGCTT CTGTCATCTT GAGCATAAGA GTATCTGGG TAATCCCTGC ATTGTTGACC	360
AAAACATCTA CTGAACCCAG TTCTGCAATA GCTTGATCAA TCATACGCTT AGCGTCTGCA	420
AAATCTGATA CATCTCCTGA AATGGGAACC ACCTTGATAC CATAGTTGA AAAACTCAGCG	480
AGCAATTCTT CTGAGATTGC CCCACGACTG TTTAAGACAA TGTTGGCTCC TGCTTGAGCA	540
AACTTGTGGG CGATGGCAAG ACCAATTCCA CGACTCGAAC CTGTAATAAA GATATTTTA	600
TGTTCTAGTT TCATTTTTTT CCTTTCAAAA CTTCTACTTA TTTTAGTCTA TTTTTCTAAA	660
AGTGCTACTA AACTCGCTTG ATCTTCCACA TGAGCTAAGT GAGCAGTTG ATCAATTTT	720
TTAACAAAAC CTGACAAGAC TTTCCCCGGT CCAATCTCGA ATAAAGTTGC TTATGCCTGC	780

TTCTTGATG ACCCAATAC TTTCATAGAA ACGAACGGGT TCCTTGACCT GACGCGTCAA	840
GAGCTGAGCA ATGTCCTCTT TTTGCATCAC AGCAGCTTCT GTATTGCCGA CTAGGGGACA	900
AGTAAAATCT GAAAAACTTA CCTGAGCTAG AGTTTCAGCT AGTTTCTGGC TAGCAGGCTC	960
AAGGAGAGCG GTGTGAAAGG GACCTGACAC CTTAAGAGGA ATCAAGCGTT TGGCACCTGC	1020
TTCTTGCAAA AGTTCAACCG CTCGATCAAC TGCAACCCT TCTCCAGCAA TGACGATTTG	1080
TGCAGGTGTG TTATAGTTGG CTGGAGTAAC CACTCCAAGT TCCAGAAGCT TTTTGACAGG	1140
CTTCTTCAAT GACCTCTACT GGCGTATTGA GAACTGCTAC CATCTTGCCA AGTTCAGCA	1199

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CTACTATTTT CTTTGCCATA GCCTTCTCCT TTACACACTA CGCATATCGT GGTAAGAAC	60
ACTGCGTCCC ATCTCACCTG CATTCTCTTT TTGAACAAAG GTATTAGCGT TTATATAGGC	120
AATAGCAGAA GCCTTCAACA CATAAAATC AAGCCCTGCT GCATTAAGA TGGTTCTGT	180
ATCCCTGTT TCAACAGTGA CCAACAAACCC GATCCTGGC ATCGATTCCA TCTGTTACCG	240
CATTGATAGT GTAGGACACC AAACGAACAG ATTGGTTAAA GAACTTATCG ATAGCGTTAA	300
AGATTGCTTC AACGGAACCC TGTCCCTGTC GCATTAATT CGACTTTCTC ACCATCCATA	360
TTGGCTAGGC TAACGAGCGC TTCAATGTCA TTATCTGCAT GAGTTGAAG TTGTAATCA	420
TCAAAGTGGG AGCCTCTGG ATTTCAACC ATGGTTCCAG CTACCAAAGC TCGAGTATCT	480
GCATCTGTGA TTTCTTACTT CTTATCGGCC AGTGCCTTGA ACTTAGCAAA GAATGGTTG	540
ATATCCTCTT CTGTAAAATC TAAGGCCAT TCTCTCAGTT TCTCAACAAA AGCATGGCGA	600
CCAGATAATT TTCCAAGCGG AATCTTAACA CCAACCAATT CAGGTGTGAT GATCTCATAA	660
GTGAGAGGGAT TTTAAGGAC TCCATCTGG TGAATACCAAG ATTGTTGGGA GAAGGTATTG	720
CCACCAACGA CGGCTTGTT TTTAGGAACG GGAATACCAAG AGAAGCGAGA AACCATTCT	780
GACGTATTGA TGGTCTCATT TAGGACAATA CTGGTTCTA CTTGGTAGTA ATCTTGGCGA	840
ATATTGAGAG CCAC TGCAAT TTCTCCAAA GCAGCATTTC CAGCTCGCTC CCTAATACCA	900
TGGATAGTCT CTTCAAAAG TCCTGCACCA TTCTTGACAG CAGCAAGGCT ATTTGCCACT	960
GCCATCCGAA GTTCATCATG ACAGGGAGGC GAATAGATGA TCTGACGATC CGTCTGGACA	1020
TTCTCAATCA GGTATTGGAA GATGGCACCA CATTCTCTG GTGTGGAAA TCCTATATTT	1080
TCTGAAAATT TCTTCAGTAA AGAATATTAA GCTAATTGAA AGTTCATGAA AATTATTAAA	1140
ATATTCATT TTTTAGAGGT TAAGTTCCAA CTTTTTCTA TCAATTCCAG TACTTNTTCA	1200
TCTGATAAAAG TATCATCAAG GGACACACTA ATCCAGTAGC GCTTGCTCAT ATGGAAGGCT	1260
GGATAAAATCC CCTTTGTGA AAGCAAATTA GCTACTTGGT CATGCTTGAG GTTGACTGCT	1320
TCCACTTGTC CTTCTGTGCC CTTTTCCAGC TTATTCCAAG AGATTTCAN CAAGACGGCA	1380
TACCACTTTT GATTGCCTTC ATGGCGCAAT ACAG	1414

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

CTCCCCATTT	TGGAAAATTT	CTGTCAAGAA	ACGGCGAACCC	AGCTTTTAT	TTTCTGCTTT	60
CTTGTCCAAA	TCCTTGATTT	CAAAATCTCC	AAAAATTGAA	TCTAGTTGGT	CATTTTCAGG	120
TGTTCGATAG	TAGTCAATGA	CATCCCAATG	CTCAACAATA	CGACCATTCT	CATCCGCACG	180
GAAAGTATCC	GTCGTCACCC	ATTGAGCTTC	TCCACCATTC	AGATATTGAT	GGAACATGAA	240
CAAAGACCAAG	ATTGCCATCC	TCAATGGTGC	GGACAATCTT	AATCTGACGC	TCTGGATGAC	300
GCTCAAAGAA	ATCTGCAAAG	AAGGCTGCAA	ATCCTTCTTT	CCCGTCAGGA	ACACCTGTCG	360
AATGTTGGAT	ATAGGTATCC	CCTACAGACT	GGGCTTGAGC	CTCAGCAACT	CGTCCGTCTT	420
GAATGGCATG	GATGTATAGG	TTGTGAGCAT	TTTCACTTG	TTGTGACATA	TTCTAAACCT	480
CATTTCCCTT	CTCTTTCAGA	TTCGCCAAAA	TTCTTTCTTG	AAAACCTTCA	AATTGGTGAA	540
TTTCTTCCTC	TGAAAATCCT	TTGTAAAAGA	TAGTATCCAA	TTTCTGACTG	ACACGATGCC	600
CCACTTCTTT	CTGGGACTTG	CCTAACCTCCG	TTAAAACCTAA	ATACTTCTTA	CGCTTGTCTT	660
TTCCACACGG	ACTAACAAATT	ACAAGCTTTT	GTTCCTCTAG	CTTTTTATC	ATAGTCGTCA	720
CGGTATTATT	CGCAAGCCC	GTGCAAGCG				750

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 953 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GTATCGTTCA	ATTCCAAAGA	TACGGAGGAA	GCTGCGTTTC	GCGAGAAAAC	TCTTGTAGA	60
CCAGATAGGG	ATTAGCCAAA	ATCCTTCTAT	GNNGCTTATAT	CCAAATGGAG	ATGCAAACCT	120
CTGCCCAACT	CTTGACCAAT	AAGATCTTTC	TTAAAAATCC	ACTCAAGGCT	CTGGTAGAGG	180
AAAAATATGG	GATTGAGTAT	GAAGAATTAA	CCAATCCTTG	GCACGCTGCC	ATTCTAGCT	240
TCGTTGCCTT	TTTCCTTAA	AGTTTGCTC	CAATGCTGTC	AGTGACCATA	TTCCCAAGTG	300

AATATCGCAT CCCTGCTACT GTCCTTATTG TCGGTGTGGC CCTTCTTCTC ACTGGTTACA	360
CTAGTGCCAG ACTTGGAAAG GATCCGACTA GAACAGCTAT GATTGGAAC CTTGCTATTG	420
GTCTCTTGAC CATGGGAGTT ACCTTCCTGC TCGAACAACT TTTCAGCATT TAGAATACAA	480
GAAATACCTC GATTTGAAG TCGAGGTATC TTTTTTACAT TTGCACAATC TTGCGATAAC	540
TTCTTGAACT AATCATGAAA ATCAGCACAT AGGCGATGAG GAAGATAGCG CAGATAGACA	600
AGGTCACAAT CAACATCATA GTCGTATCCA GTACACCAAT CACTTTAAA ATCAGGCTAA	660
GCATATGGTA GGCAAAGGCG AGATGTATGA AGGCAAAGAG CAAAGGAAGG AAGAAAACAG	720
TTAAAACCTG TTTGTTGATG GTTTGCTTGA TTTGCTTTG GTCCAAACCG ACTTTCTGCA	780
AGATAATAAA GCGTTCACGG TCTTCGTAGC CTTCAGAAAT TTGTTTAG TAGATGACCA	840
GAACAGTTCC GACCATAAAG ATAATGGATA GGAAAATACC GATAAAGAAG ACACCGCCAA	900
AGAGGACACT CATTGAGCA CTAGCATCTG CTAGATTGCT ACCATAAAACA TAG	953

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 665 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CTGATTGAACTTCTATTTAC TAATATTCAA AAATCCTCCG TTTCAAAGAG CAGGGAACTC	60
TTTGTGACAG AGGATTTTT CTATAGGGCT TTAGCAGCTG CAATTGCGGC TTCGAAGTTT	120
GGCTCAGAAT TGATATTATC CACGTATTCA ACGTAGCGAA TCGTATTGTC AGTATCGAGG	180
ACAAAGACTG CGCGTGCTAA TAGGTGCCAT TCGTTGATCA AGAGGGCATA ATCGCGCCCG	240
AAAGAATGGT CAAAGTAGTC TGAAAGCATA ATGGCATTGT CAAGGCCCTTC AGCACCGCAC	300
CAACGTTTT GAGCAAAGG TAGGTCCATT GAAACAGTCA ATACGACCGT GTTGTCCAGT	360
CCAGCCAATT CTTCATTAAA ACGACGTGTT TGAGTTGAGC AGATGCCGT ATCGATAGAA	420
GGAACGACAC TCAAGACTTT TTTCTTGCCA TCAAAATCAG CCAGAGATTT TTTAGAAAGA	480
TCTGTTGTAG TAAGAGAAA ATCAAGCGCC TTGTCGCCGA CTTGTAGTTG TTTACCTGTA	540
AAGCTCACAG GATTCCGAG AAAAGTTACC ATAGGATACT CCAATCTTT TTCTTCCATT	600
GTATCTGAAA CAGTCAGAAT TTTCCAATGA TTTGACCGGA AATGTGGCA TAGAAAAAAC	660
GCCAG	665

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1039 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

CTAAGTATAA AAAACTTGCC GAAAGTATCT CTGAAGTTAA TTTGAATGTC	TTTTTTCAAA	60
ATGCTTTAGA TTTGTGAA ATCTTTAAC CAAAGGCCTTG TCTGATAAAAT	TTTTTTGAGT	120
TTATGAATT C TATGTTACAA GGCGATATT CAAAGTTAAC AATAAACCAA	GAATAATAAG	180
AGGGGAACAG TATGAAAGAT ACGATTCTA ATAAGGATT GATTCCATG	GGCTATAGAC	240
CATCAACAGC AAATGCTATT ATCCATCAGG TGAGAGAATT ACTTGTATCA	CGAGGCTATA	300
CATTTTATAA TCGCAAACGT TTGATGGTTG TTCCAAAAAG TGTTGTGAAA	GAGTTGTTGG	360
GAATGGAATT GTGAAATGGC TTATATCGAG TATAAACAGC GTGGGAAGAA	AAGGCTTGG	420
TCGTTTCTA TACGTGAGAG GAGCAAGAGC CTACTCCATA AAAGCGGATT	TAAAACAAAA	480
CGAGAACGTA AAATAGAACG GGAGAAAGTT CTTCATAAGT TAAATACTGG	GAGTGTCTTA	540
AGCTCTAGTA TGACTTTATC GGAGCTTTAT AATGAATGGC TGGATTAAA	AATTTACCT	600
AGCAATAGAA GTGTAGTTAC TAAAAAAAAA TATCTTATGA GAAAGAAGGT	CATCGAAAGG	660
TTATTTGAA ATAAGCCTGT ATCACAAATT AAGCCTAGCG AGTATCAAA	AATTATGAAT	720
GAGTATGGAG AGACTGTATC GAGAAATTTC TTAGGAAGAT TGAATTCTAG	TATCCAGGCA	780
AGTATACAGA TGGCTATTGC TGATAAGGTG ATAATAGAGG ATTTACTGC	TTATGTTGAG	840
TTGTTCTCTT CTAAGAGTGG ACACAAAGGT TGAGGAAAAG TATCTACATA	CTGAGTCAGA	900
TTATCAAAAA GTTTAGTAT ATTTGAAAAA TAAGTTTGAT TATCAGAAAT	CTATTGTACC	960
GTATGTAATT TATTTCCCTT TTAAAACCTGG CATCGTTTC TCCGAATTGA	TTGCTCTAAC	1020
TTGGGATGAA GTTGACGAG		1039

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

CTGAGAACGTC AGGAAGGCGA TGTGGAGAGA TTGAGGAATT GGATACTTAA	CTCCATAGTA	60
ATCTTCGTA AACTCGATAG AGCGAACAGC GATATCCAGT GAGAAATCAA	GATTGAAAG	120
TGGATGTGCT TTGGTTGAGT AGACACCCCA CCAGGGTACC ATTTTTAGTT	TTAGCGGTCA	180
CCCCCTTGCAA ATCACCCAGCA ACAAAAGGCCA ACAAGTAAGA AGACATGCGA	GGTGTGTC	240
CAAACCTCCA GATACCTGTT TCCTTACGGT TTTCAACATC GATTCTGGC	ATGTTGACA	300
AGGCCAATTC ACCTTCTGCT TGGTCAAAGC GAAGAGAGAG GTCAAAAGTT	GCTTTGGCTT	360
CAGGCTCATC CACACATGGG AAAGCTTCGC GCGCAAATG GCTCTCGAAC	TGAGTAGACA	420
AGACCTCCCTT CTTGACTCCA TCAACTGTAT AATAAGAACG GTAAATCCCT	GTCATGTTGT	480

CTGTAATTT ACCAGAAAAG GCAAGAACCA ATTCAACTTG ACCAGCCTCA GCCAATTGCA	540
TATGAAGGGC TTCATTGTCA TGGTCAACTG TAAATGGACG AGCTTGACCT GCAACTTCTA	600
CAGAGGTGAT TTCCAAGTCT TTTTGGTGGA GGGAGATGCG GTCACTCTGT GCTTGACCAG	660
TGATGGTCAC TTTCCCAGAA AAAGTCTTGG TCTCACGACT CAAATCTAAA AATAAATCAT	720
AATGTTCAAG AACAAATTGC TTAATAAAAT GTTCAACTGC TTGCATAGTT TTCTCCTATT	780
CTAAGTTAA GAG	793

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

CGGATGATTG GCTTTTCATC TATGATAAAAG TCTTTGTTGA GCGTCGGAAT CTCTACTGAC	60
TGGAAATTTC CCGTAGATAA TCCAAATGCC CTTTAAAGAA AACCTCATCT GTCAACACCG	120
AAATCATCAC TGCTCCGTTT TCTTCATAAG TCTGGGCCTG TTGCACAATA TCCACATCGA	180
GATTGATATC TCCCCAAAAC TAGGGCTAGC TTTCTTGACT TCAGCGATTA CCTGCAAGCG	240
GTCCTGATGA TTCTTCAAAAA ATTCTGCCAA GCGATAGGTC TGGCGCAGAG GCTGGATTG	300
CTCCAGCTTC ATCTGCTCCA CCTCACGCGC CTTCTGCTCT AAGATTGCGT CTAAAAATTG	360
CTGACTCATTT TTTGGTACTC CTGTAACAGT CTGAGTTTTT CAAGGGCCTT GCCTCTAGCA	420
ATCACTTGAC GGGCCAAGGC AACTCCTTCC TTGATGCTAT CAATCTTACC ATTAGCATAG	480
AAACCAAGAC CAGCATTCAA GACTGTCGTT TCCAAGAATG GACTTGCTTC GTTTTCAGA	540
ACGCTAAGCA AAATTCTGC ATTTTCTGA GCATTCCCAC CACGAATATC TTCCATAGCA	600
TAGCCTTCCA TTCCCAAATC CTCTGGAGTA AAGCTTGACA AG	642

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 733 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

CTCTTGCAGG TTATTAAGGA GAAAACGGAG GTAATAGAAG TATGATTAT ACAGTCACAC

60

TCAATCCATC CATTGACTAT ATCGTTCGTT TGGACCAAGT CAAAGTTGGT AGTGTAATC	120
GTATGGACAG TGATGATAAG TTTGCTGGTG GGAAAGGAAT CAATGTCAGC CGTGTCTTGA	180
AACGTTGAA TATATCAAAT ACAGCGACGG GATTTATCGG TGGCTTTACT GGTAAATTAA	240
NCNCAGATAAC TTTAGCAGAG GAAGAAATCG AGACNCGTTT TGTCAGGTG GCAGAAGATA	300
CTCGTATCAA TGTAAAATC NAAGCAGACC AAGAACAGA AATCAACCGA ACGGGTCCAA	360
CTGTTGAACC GGTAAAGCTA GAAGAATTGA AAGCTATTTT ATCTAGTCTG ACAGCAGAAG	420
ATACAGTTGT CTTTGCAGGT TCAAGTGCTA AAAATCTAGG CAATGTTATC TATAAGGGAT	480
TTAATCTCCT TGACGCGCCA GACTGGTGC CGAAGTGGTCT GTGACTTTGA AGGACAGACC	540
TTAATTGATA GTTTGGATTA CCACCCCTCTT CTTGAAAAC CAAATAATCA TGAACTTGGA	600
GCGATTTTG GGGTTAAACT CGAAAGTTTA GATGAAATTG AGAAATACGC TCGTGAGTTA	660
CTGGCTAAGG GTGCTCAAAA TGTTATTATC TCTATGGCTG GTGATGGTGC CCTTCTTGTC	720
ACATCTGAGG GAG	733

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

CTAAGGGAAG TAGGAAAAGT ATGTATCCAG ATGATAGTTT GACATTGCAA CACGGACTTG	60
TACCAAGATCA ACATGATGCA GGTTTACTTT GATCAAGGGA TTTACAATAA GAAGGCGGTC	120
TTTGAGGTGT ATTTCCGCCA ACAGCCTTTT AAGAACGGCT ATGCCGTTTT TGCAGGTTTG	180
GAAAGAATTG TGAACATATCT TGAAGACTTG CGTTTTTCAG ATAGTGATAT AGCCTATTTG	240
GAGTCGCTTG GTTATCATGG GGC GTTCTTG GATTACCTTC GCAATTCAA GTTGGAGTTG	300
ACCGTTCGTT CTGCCCAAGA AGGGGATTG GTTTTGCTA ATGAACCGAT TGTGCAGGTG	360
GAAGGACCTC TAGCCCAATG TCAGTTGGTC GAAACGGCTC TTTTGAACAT CGTCAACTAC	420
CAGACCTTGG TGGCGACGAA GGCAGCCCCC TATCCGTTTG GTTATCGAAA ATGAACCCCTT	480
GATGGAGTTT GGGACACGTC GGGCTCAAGA AATGGATGCG GCCATCTGGG AACACG	536

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CTGCCCTGT AAGGCTGGAC GATTGCCTTT CTTAGTATCC GCAAAGAGGT AAACTGAGAA	60
TAGAGAGGAT TTCTCCTTCA ATATCTTGAG CAGACAGGTT CATCTTGCCT TCTACGTCCTG	120
AAAAAATCCG CATATTGACC AGTTTCTCA CAGCATAGTC CAAATCTTCC TCTTGGTCCT	180
CTGGTCCAAC ACCAACCCAGC AATAAAAGTC CCTGATTGAT TTTCCCTGA ATCTGGCCTT	240
CTATACTCAC TTGGCTTTT TTAACCCGTT GGATAATGAT TTTCATAATA GCCTTCTAG	300
TAAGAGCTAG GACAACTAGC CGTTGGTCCG TTTGACAGAG TAAACTTCTG GCACACTCTT	360
AATTTTATCG ACAACCGTGG TCAGTGTAGA GAGGTTGGCA ATACCGAAGG ACACATGGAT	420
ATTAGCAAAC TTCATATCCT TGGTTGGTIG GGCATTGACC GTTGAATAT TCTTGGTTGT	480
ATTTGAAAGA ACTTGCAGTA CATCGTCAA CAGTCCTGTA CGGTTGAGAC CGTAGATATC	540
GATATGGGCC ATATACTCCT TATTGAG	568

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

CTTTATATTG TACCAAGTAT CATTCTAGT GCTGCTATGG GCTTGATTTT TCTTCAAATC	60
TATAATCCAA ACTATGGTGT TGTTAACCAA ATTATTCACT TATTTAATCC ATCGTTAAA	120
GATTCACTAC TGTTGACTCC CAGGATTAAA AATAGTAGCT ATGACTGGCG CTTATATCTT	180
CTTTGCAGGA GCATCAACCA TTATGATTT TCAGGCAAAT TTTGCTATT CCAGAAGAAG	240
TTCAAGAACG TGCTATTTA GACAATATTA CTGGTTGGAG GAAAGAGTGG TATATTACGA	300
TTCCGATGAT TAAGGGACA ATTAAAATG TTTCAATTAT GGCAGCACT TCAGGATTTT	360
TGCTCTATAA CGAAGTATTC TTTTGACAA ATGGTGCTGC AGGAACAAAA AGTATCAGTT	420
TTGTTATTG AGAATTAGCA GTGGCTAGCT CACGAACCTCA GTATGCTCGT GCAAATACAA	480
TTGGAGTTAT ACAATCTTA GGTGGAATGT TGATTATCGT TTGTATTAAT ATTTTATTCA	540
GAGAAAGAAA AAGACTGAAA GGTGGAAAT GATTATGAAT ACACATATAA ATGGTATTAG	600
AAAAAAAGGC AAAGTTCTTA TATATGGTTA TATGCTCCTT ACCATTTAA TTTCTATTTT	660
CCCTATTGCG TGGATTTTT TATCATCATT AAAAGCAGAT CCTATGAAAA ATCCAGGTAT	720
TAGTTTACCG ACTGACTTTA CTCTTGAAGG TTATATAAT GTTTTACAA AACTTCATGT	780
TTTTACTTAC TTTTGGAAATA	800

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 686 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CTCAGTATTA TCCCTACCAA AATGAACGTC AGTTAGTGAC TCAGGTGGTT TGGGAACAAT	60
GGGCTTTGGA ATTCCAGCAG CAATCGGTGC TAAAATTGCT AACCCAGATA AGGAAGTAGT	120
CTTGTGTTGGT GGGGATGGTG GTTCCAAAT GACCAACCAG GAGTTGGCTA TTTTGAAATAT	180
TTACAAGGTG CCAATCAAGG TGTTATGCT GAACAATCAT TCACCTGGAA TGTTTCGCCA	240
GTGGCAGGAA TCCTTCTATG AAGGCAGAAC ATCAGAGTCG GTCTTGATA CCCTTCCTGA	300
TTTCCAATTG ATGGCGCAGG CTTATGGTAT TAAAAACTAT AAGTTTGACA ATCCTGAGAC	360
CTTGGCTCAA GACCTTGAAG CTACTACTGA GGATGTTCCCT ATGCTAATTG AGGTAGATAT	420
TTCTCGTAAG GAACAGGTGT TACCAATGGT ACCGGCTGGT AAGAGTAATC ATGAGATGTT	480
GGGGGTGAAG TTCCATGCGT AGAATGTTAA CAGCAAAACT ACAAAATCGT TCAGGAGTAC	540
TCAATCGCTT TACAGGTGTC CTATCTCGTC GTCAGGTTAA TATTGAAAGC ATCTCTGTTG	600
GAGCAACAGA AGATCCGAAT GTATCGCGTA TCACTATTAT CATTGATGTT GCTTCTCATG	660
ATGAAGTGGGA GCAAATCATC AAACAG	686

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TTTTCCCAGC TATTTTACTG ACTATAAAAG CCTTATTTAA CTTACTCTAT GTACTCGGTT	60
TTCTAGGAGG AATGTTGGGA GTTGGGATTG CTTTGGGGTA CGGAGTGGCC TTATTTGACA	120
AGGTTCGGGT GCCTCAAACA GAAGAATTGG TGAATCAGGT CAAGGACATC TCTTCTATTT	180
CACAGATTAC CTATTGGAC GGGACGGTGA TTGCTTCCAT AGAGAGTGAT TTGTTGCGCA	240
CTTCTATCTC ATCTGAGCAA ATTTGGAAA ATCTGAAGAA GGCTATCATT GCGACAGAAG	300
ATGAACACTT TAAAGAACAT AAGGGTGTAC TACCCAAAGGC GGTGATTCGT GCGACCTTGG	360
GGAAATTGT AGGTTGGGT TCCTCTAGTG GGGGTTCAAC CTTGACCCAG CAACTAATTA	420
AACAGCAGGT GGTTGGGAT GCGCCGACCT TGGCTCGTAA GGCAGGAGAA ATTGTGGATG	480
CTCTTGCCTT GGAACGCGCC ATGAATAAG ATGAGATTAA AACGACCTAT CTCATGTGG	540
CTCCCTTGGG ATCGAAATAA TAAGGGACAG AATATTGCAG GGGCTCGGCA AGCAGCTGAG	600

GGAATTTTCG GTGTAGATGC CAGTCAGTTG ACTGTTCCCTC AAGCAGCATT TTTAGCAGGA	660
CTTCCACAGA GTCCCATTAC TTACTCTCCT TATGAAAATA CTGGGAATT GAAGAATTGA	720
TGAAGACCTA GAAATTGGCT TAAGACGGGC TAAGGCATTC TTTACAGTAT GTATCCTACA	780
GGTGCATTA GCAAAGACAA TT	802

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 545 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CTACTATTT AGCATAAAAA TGCCCCAAGG GGGNGCCGTG TGTTTACTGA TTTTCAGGNT	60
AATGGACCAG GNAAATCAGC ATGAAAATAA AAAGAGAAC AGATTATTTT AGCCATTG	120
CAGATTTATG CTATGCTTAA GGTAGAAAAT GAAAGGGATA ACAAAATGTAT TTAGGAGATT	180
TGATGGAGAA AGCCGAGTGT GGTCAATTAA CAATCCTTTC CTTTCTATTAA CAAGAGTC	240
AGACGACCGT CAAGGCTGTA ATGGAAGAAA CAGGATTTTC AAAAGCAACC CTAACCAAAT	300
ATGTCACCCCT GCTCAATGAC AAGGCTTTGG ATAGTGGCTT AGAACTGACT ATTCACTCAG	360
AAGATGAAAAA TCTGCGTCTG TCTATAGGTG CAGCTACTAA GGGGAGAGAT ATTCCGGAGC	420
TTGTTTTTG GATAGTGTG TTAAATACCA GATTTGGTT TATCTTCTCT ACCACCAACA	480
GTTTTTAGCC CATCAGCTGG CTCAGAATT GGTGATTAGC GAGGCTACGC TTGGTCGTCA	540
CTTAG	545

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 576 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GAGGTCAAGA TTGATTCCCA AGGTTNGAGG AATCTGCGGA ACCAGATTAA GAAGAAATCG	60
AGCGGTTACC ATGCTTGGCC ATGTGAATAC CGCCACCAGC CAAGACAAAG GCTGCAGTTG	120
TGGAAATATT AAAACTGAAA GACTTGTCCC CACCTGTACC ACAGTTGTCC ATAGCATCAT	180
GAATCTCAGT TGGAAATATGC TGGGCATGTC CTCTCATGAC TTGGGCAATG GCTGTGCGTT	240

CTTCAGGTGT TTCCCCCTTC ATCTTAAGAG CTAAGAGGAG AGAAGCAATC TGCGCTTCAG	300
TTACACGCC AGTTACGATA CGCTCAATGA CATCCGTCAT TTCCACACCT GATAAATTTC	360
CAAATTTGC TAGTTTTCA ATAATCTCTT TCATCCTAGT TTCCTCACCT TACAACCTCC	420
TCGATAAAAT TCCGAATAGA AGACAAGCCG TCTGGCGTTC CAATGCTCTC TGGATGGTAC	480
TGGAAGCCAT AAATCGGTAG GTTTTATGT TGAATCCCCA TGATGGCTTG GTCATCAGTC	540
GAACGAGATC AAGCTTATCG ATACCGTNGA CCTCGA	576

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 669 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATTAAGGGGA GGCGAACATG GCCCAAGATA TAAAAAATGG AGAAGTAGAA GAAGTTCAAG	60
AAGAGGAAGT TGTGGAAACA GCTGAAGAAA CAACTCCTGA AAAGTCTGAG TTGGACTTGG	120
CAAATGAACG TGCAAGATGAG TTCAAAACA AATATTCTTC GCGCTCATGC AGAAATGCAA	180
AATATCCAAC GCCGTGCCAA TGAAGAACGT CAAAACCTGC AACGTTATCG TAGCCAGGAC	240
TTGGCAAAAG CAATCTTACC ATCTCTTGAC AACCTTGAGC GTGCACTTGC AGTTGAAGGT	300
TTGACAGATG ATGTGAAGAA GGGCTTGGGG ATGGTGCAAG AAAGCTTGAT TCACGCTTG	360
AAAGAAGAAG GAATTGAAGA AATCGCAGCA GATGGCGAAT TTGACCATAA CTACCATATG	420
GCCATCCAAA CTCTCCCAGC AGACGATGAC CACCCAGTAG ATACCATCGC CCAAGTCTTT	480
CAAAAGGCT ACAAACTCCA TGACCGCATC CTACGCCAG CAATGGTAGT GGTGTATAAC	540
TAAGATACAA AGCCCGTAAA AAGCTCGCAG TAAAAATAGG AGATTGACGA AGTGTTCGAT	600
GAACACAAAGA AAATCTANCT TTTTACTCA GAGCTTAGGG CGTGTTCGAT TCGGCAATTG	660
TGACGGTAG	669

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

CTAGTTCA	CC ATTTCTATTT	AAATTGGCT	CAACTACACC	GAAATATCAT	ATAAGGTA	AA	60
GTTCCC	ACTA AGAATCTCAG	AATGAAATTC	TTCACTA	ACT TCAGCGGTCA	AACTTAGCTT		120
ATCCAAT	TTTC AGACCGATAA	ACCCATACTT	CAGAGATACT	TCCTCTTGAA	ATTTAGAGTA		180
ACTCTT	TATTA GACATTTGAT	GTATCGTTAT	CGGGCTATTA	GAAGGAGCCC	GATTTAAAAC		240
TTCTT	TATTC ATGAAATTC	TCCTTCAAAA	AACAAAACAT	TCTATATACT	TAAATTTAG		300
GGCAAG	ACTG CCGTTCCACT	GACCACGCTC	CACTTGCCAG	CAAAGCTGGC	AGGTCCAGCC		360
TTACCC	TAAATTAT TTAATT	TTG CCATTTCAAT	CAATTCTGCA	AAGGTCCCAA		420	
GCTT	TCTGGA TTGAATTACC	TCATATTGGG	CATTCTGTCC	AAATGAAGCA	TTATTAAATCA		480
CTTC	AACCTC ATAAGGCCT	GGAGCAGAGA	AAACAGCTCC	AAATTGGAT	TTATCGAAAT		540
GCATA	ACCTAG GTCACTCCAA	CAATCATTAA	GGGTGGAGAC	TTTATCCAG	CCTCGTTCTT		600
TCTT	AGTAGA AATAG						615

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CTACTGTAGT	TGGAAC	TGTT GAAAAACAAG	GAAAACAAA	GAAAGTTGTT	ACTTACAAGT		60
ACAAAC	CTAA AAAAGGTAGC	CACCGTAAAC	AAGGTCA	CCG TCAACC	ATAT ACAAAAGTTG		120
TCATCA	ACGC AATT AACGCT	TAATT	TTAAG GAGAACACAT	GATA CAAGCA	GTCTTGAGA		180
GAGCCG	GAAGA TGGCGAGCTG	AGGAGTGC	GG AAATTACTGG	ACACGCCGAG	AGTGGCGAAT		240
ACGGC	TTAGA TGTGGTGTGT	GCATCGGTTT	CTACGCC	TGTC ATTGC	CATTAAC	TTT ATCAATTCTA	300
TTGAGAA	ATT TGCAGGCTAT	GAACCAATCC	TAGAATTAAA	CGAAGATGAA	GGTGGCTATC		360
TGATGG	TGTGA AATACCAAAA	GATCTCCTT	CACACCAGAG	AGAAATGACC	CAGTTATTCT		420
TTGAAT	CATT TTTCTTAGGT	ATGGCAA	ACT TATCGGAGAA	CTCTTGAG	TTCGTCCAAA		480
CCAGAG	TAT TAT CAGTTAT	CACAGAAAAC	TAACACGGAG	GAAAACATTA	TGTTAAAAT	GACTCTAAC	540
AACTTG	CAAC TTTTCGCCC	CAAAAAGGT	GGAGGTTCTA	CATCAAACGG	ACGTGATTCA		600
CAAGCG	AAAC GTCTGGAGC	TAAAGCAGCT	GACGGACAAA	CTGTAACAGG	TGGATCAATC		660
CTTTACCGTC	AACGTGGTAC	ACACATCTAT	CCAGGTGTAA	ACGTTGGTCG	TGGTGGAGAC		720
GATACCTTGT	TCGCTAAAGT	TGAAGGCC	TA GTACGCTTTG	AACGTAAAGG	ACG		773

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 713 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CTGGATAATT GGAGCAATT C	TGATGCCAG TTTGAGGTTA CTGATAGGAT TGTGGCGAT	60
AGCCACTTGA GAAGATGCCA AGACTCTCAAT TTCTCTCTCG TTTAATTGCA CCCCGTGAGC	120	
AAATACGGAC GGATGATCTA AATAACCCAG TTCTTCAGA AAAGCAAGGG GGCCTTGCC	180	
GTACCGTTG AGGATAATT C	CTGACTCCTC CTTGGTCTCC GCCACATGGA CATGGAGCGG	240
AATATTTAGC TCTTTGCCA TTTCCAAA	ACT CGCTTCCAGC AAGTCTCTAC TGCA	300
CGGAGAATGA GGTGCTACCA TAACCCCTGA AATTGAGGAT TTTTATATTT TAAGATTTCG	360	
TCTATGATGG ATCGAGTTCT GCTTATAGTC TCAGCAGTTG TTTCTGTCTC TGAAGAAAAG	420	
AGAGTCGGAG AAAAATAACA ACGCATCTTGAAGTTTCA CCACCTGATA AATTGCTGG	480	
ATATCCACAC CATTGGGATT ATACATATCG TTAAAGGTTG TTGTTCCCTGA CTGGAGCATC	540	
TCTGTTAGGG CTTCTTGAC CGCATTGGTA GTCATGTCGG GAGTAAACTC AGATTCTGCT	600	
GGCCAGATAT AGTCATTGAG CCATTCATG GAGATTGCTG TCATCTCGGA TCCCTCTCAG	660	
ACCTGTCATT GCAGAATGGG TGTGACAATT GACCAAACCA GGCATAAGCC AAG	713	

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

CTAGAAAATC TGCTTTTTC TCGAAAAGTT TAATACTTGG TACAATATTA CGCTTGCTTT	60
GCTCCGGCTGC TCCAAGGGCA ATTTTTCTA GTTTTTCAAC TTTTTTACCC AATTCTTGC	120
CATCCCACCTT GGCAACTGAC CAGTCTGCAG GAAAGGCCA GATTGGCTA GCACCCAGTT	180
CGGTTACTTT TTGAGCGATG AACTCCAGCT TGTCTCCCTT GGGAAATCCA GATGCGATGG	240
TCACCTGGAC TGGTAGTTCC ACATTGTCAT TTAATTCTTG GACCAACTCA AACTGACGAT	300
TTTCCATATC CAGCACGCGC GCCAACCGCT TGATGCCATC ATCAAAGACT AAGGTAACCT	360
CATCCTCTTC TTTCAAGCGC ATAACCTGAA ACATATGCTT ACTGGTTTCC TTGTCCTCGA	420
TAGTGACAGG AGAGATAGCA CTGCCTTTA CAAAATACTG CTGCATGCTA GCCTCCAATC	480
ACACCAAGAGA TATCCTTGGT TTTCTTAAAG ACACAGGTAT TCCATTCCCC TTGAACCATG	540
TGAGTTTCA GGAAAAATCC AGCTGATTCA GCCGACTCGC GCACCATGTC CCACTTATGC	600
CTTGAATAAT GCCACTCATG ATCAGGTAGC CTTCGTCCTT AACCAAACGA TAGGCATCGT	660
CTATTAGATG AATGAGGATA TCCGCCAAGA TATTAGCCAC AATCACATCT GCCTCAATT	720
CCACACCCCTT AAGCAAATCT CCAGCCGCTA CATGGATATT TTCCATGCCA GGGTTGAG	778

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1062 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

CTTCCCAGAT	TTTTCGTTG	ACTTGCTGTT	CAATCGCACG	CAATTCTTCA	GCAGTTACAG	60
CTTGGAAAGTG	GGTAAAGTCA	AAGCGAAGGA	ATTCAACTTC	GTTAAGAGAT	CCTGCCTGTG	120
TTGCGTGGTT	TCCAAGGATA	TTGTGAAGGG	CAGCGTGAAG	CAAATGAGTC	GCAGTGTGGT	180
TTTTCATGAC	ACGGTGACGG	CGATTGCTAT	CAATTGCCAA	GGTATATTCT	TGGTTCAAGG	240
CAAGCGGTGC	AAGGACTTCA	ACTGTATGAA	GGGCTTGACC	ATTTGGGGCT	TTCTGAACAT	300
TGGTCACAGT	AGCCACAAACC	TTACCTGACT	CATCCAAGAT	TTGTCCGTAG	TCAGCTACCT	360
GTCCACCCAT	TTCAGCATAA	AATGACGTTT	CCCGCAAAGA	TAAGAGAGGC	AGTTCCCTTCT	420
GAAACAGCTT	CTACTTCTGC	ATTGTCCGCC	ACGAATAGCT	ACCAATTAG	AAGACAATTG	480
GCTAGCATTG	TAGTTGAAGG	CACTTTCTAC	AGTGATGTTT	TGAAGAGTTT	CCATTTGCA	540
TACCCATTGA	GCCACCCCTG	ACAGCTGACG	CACGCGCGC	TTCTTGTGTT	TCTTCATGG	600
CTGCTTCAAA	ACCTTCACGG	TCTACAGTCA	TACCAGCTTC	TTCAGCGATT	TCTTCAGTCA	660
ATTCAACTGG	GAACCCATAA	GTATCATAGA	GTITGAAGAC	ATCTGAACCA	GCGATAACAG	720
ATTGACCTTT	TTCTTCAAG	TCTGCTACAA	TGCCCTGGGC	AAAGTGTGA	CCTTGAGTGA	780
AGGGTACGGG	CAAATGATTC	TTCTTCGCCCT	CTTAACGATT	TTCTCAATAA	AGTCACGTTT	840
CTCAAGCACT	TCTGGGTAGT	AGCTTCCAT	GATTTTCCA	ACAGTTGGAA	CGAGTTTGT	900
AAAGGAAAGG	CTCGTTGATA	CCCAATTGCA	GACCCATGCA	TAGAAGCACG	ACGGAGAAGA	960
CGACGAAAGG	ACATAACCAC	GACCCTCCAT	TTCTGGAAG	GGCACCATCC	ACCGATGGCA	1020
AATGAAAGTG	AACGGATGTT	GGTCCCGCAA	TGAACCTTGA	AT		1062

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 865 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

CTCAAAGGTC	GCACCTGCAA	TACGACCCGC	TACAGGACCT	ACACTTGCTC	CATGCTTGGG	60
ACTATTGCCT	ACATAACTAC	CAAAGTCATC	AAATCCAAG	ATAACATTGG	CAAAATTTC	120
AGCCTTGTCA	GGTGCACAT	AGCGCAAGAT	AGTCGCACCA	TAAGTCATAA	CCTCAAGTTG	180
GTAGCCACCG	TCTGTCTCAA	ATCGATAGGC	CAAGACATCC	TCACCCCTCAA	CATTTCCAAA	240
TACACGCTCT	GTGTATGCTT	TCATTCTGTT	CTCCTTTAC	TATTTCTCTC	AAGCAAACAA	300
ACCATAGAAA	GCGTACTGAC	AATCTATGGT	TTATCTGATA	ATTTACAAT	CCTCTTGTCA	360
AGAATTCTATA	AACACTGTCT	TACTTTGAT	ATTCGTGAAT	TATGACACCT	TGTACTACAC	420
GGTTTACTGT	ACCTGTAGGA	GACGGTGTAT	CTGGTTTATT	TTCTACCTTG	AGTGAAGTCA	480
ATAGGGCAAA	GAGTTGGCA	AAAACGATGT	AAGGGAAGAC	ACGGTAAATA	TCATTCAAGA	540
CACCGCCACA	ACCAAGGGCC	ACTTCTTGA	CATTTCAAG	ACCAAAAGCT	TGATCACTCA	600
AAAGCACAAC	ACGACGAGCA	ATCTGGTCAC	CAGCAACTTC	ACGAACCAAG	TCCAAGTCGT	660
ACTTACGAGT	GTAGTCCGTC	CTTGTACCAA	AGAACAAAAC	AACTGTATTG	TCGTTGATAA	720
GATATTGGA	CCGTGACGGA	ACCAACTGGG	CTTTCATACA	TGGTCGCAAC	TTGAACAACA	780
GTAAATCCA	AATCTTGAGC	TGAGCCTCAT	GAGCAGTCCA	AAGAAGACCA	GCGCCTAGAA	840
GAGACCGGTT	AAGTCTTAAT	CACAG				865

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 946 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TTTGCTCCA	GTTGATAAGA	AAGGCTTGGT	CGATGTTGAG	GCGTTAGCAG	GTTTGATACG	60
GCCTGATACA	ATCCTCGTTT	CCCATCATGG	CTGTGAACAA	TGAAATCGGC	TCTATCCAAC	120
CNATTGAGGC	TATTCAGAA	TTCTTGGCAG	ACAAGCCGAC	TATTCCTTC	CACGTTGATG	180
CGGTTCAAGGC	GCTTGCCAAA	ATTCCGACTG	AAAAGTATCT	GACAGAACGG	GTGGATTGCG	240
CGACCTCTC	GAGTCATAAA	TTTCATGGTG	TCCGTGGTGT	TGGCTTGTC	TATATCAAAT	300
CTGGCAAGAA	GATTACACCT	CTTCTTACAG	GTGGTGGCCA	GGAGCGAGAT	TATCGTTCGA	360
CAACTGAAAA	TGTGGCAGGG	ATTGCAGCGA	CAGCCAAGGC	TCTCCGTTA	TCTATGGAAA	420
AGCTAGATAT	CTTTAGGAGC	AAGACTGGC	AGATGAAGGC	AGTGATTAC	CAAGCTCTTC	480
TGAACATATCC	GGATATTTTT	GTCTTTCAG	ATGAGGAAGA	CTTTGCACCT	CATATTCTGA	540
CTTTTGGAAAT	CAAAGGTGTT	CGAGGTGAAG	TCATCGTTCA	CGCCTTGAA	GACTATGATA	600
TTTCATCTC	AACAACCTCA	GCTTGTTCAT	CTAAGGCAGG	AAAACCAGCC	GGTACCTTGA	660
TTGCCATGGG	AGTGGACAAA	GATAAGGCCA	AGTCAGCTGT	GCGTCTTAGC	CTAGACTTGG	720
AAAATGATAT	GAGTCAGGTC	GAGCAGTTT	TGACCAAGTT	AAAATTGATT	TACAATCAA	780
CTAGAAAAGT	AAGATAGGAG	CATTGATGCA	GTATTGAGAA	ATTATGATT	GCTACGGAGA	840
GTTGTCAACC	AAGGGTTAAA	AACCGTATGC	GTTCATCAA	AAACCTCGT	AATAATATT	900
CGGACGTTT	GTCTATCTAT	ACCCAAGTTA	AGGTAACAGC	AGATCG		946

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CTTGCTCGTA ACAGGTGCTA TCCTTGGTGT CAATGTTAAC	60
CTTCCCAGAA AAAGAAATCG TTGAATTGGC AGAAGGATTG GCTAAAGAAA GTGGCGCACA	120
TGTTCTCATC ACTGAAGATG CTGATGAAGC AGTTAAAGAT GCAGACGTTTC TTTACACAGA	180
CGTTTGGGTA TCAATGGGTG AAGAAGACAA ATTGGCAGAA CGTGTAGCTC TTCTTAAACC	240
TTACCAAGTC AATATGGACT TAGTTAAAAA AGCAGGCAAT GAAAACTTGA TCTTCCTACA	300
CTGCTTGCCA GCATTCACG ATACTCACAC TGTTTATGGT AAAGACGTTG CTGAAAAATT	360
TGGTGTAGAA GAAATGGAAG TAACAGACGA AGTCTTCCGC AGCAAGTACG CTCGCCACTT	420
CGATCAAGCA GAAAACCGTA TGACACAT CAAAGCTGTT ATGGCTGCTA CACTTGGTAA	480
CCTTTATATT CCTAAAGTAT AATTTTAGAT AATAAACCGT CTACCAACAG CTATGAGGGC	540
TGCGACTAAT AG	552

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

CTAAAAAAAG TCAAGTAGAA AACGAATATT CTACTTAAC TGCACGAAAT TATTTTCAC	60
GAATGACTTC GACCTTATAT CCATCAGGGT CTTTGACAAA GTAATAGTTT GGTGCAGTTC	120
CTGGTAGACC ATTTGGCTCA GTCACTTCAT AGCCTTTGT ACTGTGCTCT TGATGAAAGTG	180
CCTCAAGATC AGGTGTACTG AGGGCGATAT GGGCAAACCC ATCACCAACC ACATACGGAC	240
CGTGATCGTA GTTATAAGTC AACTCCAAC T CATA GTCATC ACCCTCAAGA CCTAGATAGA	300
CAATCGTGAA GGCATGGTCT GGAAAATCTC TGCGACGCAA TTCTTTAAAA CCAAAAGCAT	360
CTTGATAAAA TGCAATTGAT TTTCAAGAT TTTCTACTCG TAAGCAAGTG TGTAGCATT	420
TTGAAGCCAT ATCTTCTCC TTTATTTTA AAAAGACTGG ACAATCCTGT TCCAGTCTCA	480

TCAGTTGTTA TTTACCAAGT TTTGCTTAG CT

512

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CTGGACCACA	CTATTTCTG	TGTTGGCTAT	CGTGTATGC	AAAAGGATCT	AGAAGGGACG	60
CTGGATGCTG	AAAAACTCAA	GGCTGCTGGT	GTTCCGTTCG	GCCCCGTTTT	TGGTAAAATC	120
AAAAACGGCC	AGGATCTTGT	TTTGGAAAGAC	GGAACTGAAA	TCAAGGCAGC	AGACTATATC	180
TCAGGCCAC	GTCCAGGTAA	GATTATCACT	ATTTTAGGAG	ACACTCGAAA	AACGGATGCC	240
AGTGTGCGTC	TGGCTGTCAA	TGCAGATGTC	CTAGTTCATG	AGTCCACTTA	TGGCAAGGGT	300
GATGAAAAAA	TTGCTCGTAA	CCATGGTCAC	TCAACTAATA	TGCAAGCTGC	ACAAGTAGCG	360
GTAGAACGAG	GTGCCAACG	CCTCCTACTC	AACCATATCA	GTGCCCGTTT	CCTCTCAAAA	420
GATATAAGCA	AACTCAAGAA	GGACGCTGCC	ACAATTTTG	AAAATGTCCA	TGTGGTCAAA	480
GACTTGGAAA	AAATGGAAAT	CTACCAGTCA	CAGAAAGGAT	AACTATGCCT	ACTATTCTCC	540
ATTAACCGGA	A					551

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

CCGTCATTAT	ACCTTTGTCT	ATGAAATGA	AGACCTAGTC	TATGAGGAGG	AAGTCTTATG	60
ATACAGCCAG	CAAGTTAGA	AGAATTAGCA	TCTTTAGTGG	AAAAAGCGGG	CAAGAAGGTC	120
TTCCTTTTG	TGGCAGACTG	GTGTGGCGAT	TGTCGTTATA	TTTATCCTGC	CTTACCAAGAG	180
ATTGAGGAGA	CCAATCCAGA	GTTCACCTTT	ATTGAAATGG	ACCGAGATCA	GTATATGGAT	240
TTGGCCAAAC	TCTGGGATGT	TTACGGAATT	CCTAGCCTTG	TTGTTCTAGA	AAAGGACAAG	300
GAAATTGGTC	TTTTGTCAA	TCGCGACCGT	AAAAGTAAGG	AGCAAATTAA	CGATTTTTA	360
GCAGGATTGA	AATAGGAGAA	AAAGGAAACA	ATGATTTTA	CGTATAACAA	AGAACATGTC	420

GGTGATGTCC TTATGGTCAT CGTGAAAAT AGCGGAGATG CCAAACGTGAA TGTGGAACGC	480
AAAGGCAAGG TAGCCC GTGT TTTCCCTCAAA GAAAATGGGG AAACAGTAG	529

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CTAGGATAGA CCGCTTTTA GCATTTATCT AAGCATTCCA GAGTACATGT ATCTTGCATG	60
TGCTCTTCT TTTGGGTTG AAACGATAGG AGAAGGAAAT GTTACAATTG CTTAAATCAA	120
TCGATGCTTT TGCTTGGGA CCGCCCTCT TGATTTATTG GTCGGAACAG GGATTTACCT	180
AACCATGCGG CTAGGACTCT TGCAAGGTTT GCGTCTGCCA AAGGCCTTTC AGCTTATTTT	240
TATCCAGGAT AAGGGACATG GTGATGTATC CAGTTTACA GCTTCTGTG TAACAGGCC	300
TTGGGCATTC AACTGGTTG GGAAACAGGG AAATATCCAT TAGGGAGTTG GCGACGGCTA	360
TCAAGGTTGG TGGACCAAGGA GCTCTATTT GGATGTGGAT GGCAGCTTTC TTTGGAATGG	420
CTACCAAGTA TGCGGAAGGA CTCTTGGCCA TCAAATACCG CACCAAGGAC GACCATGGTG	480
CAGTAGCGGG AGGTCCCAGT CATTATATCC TTCTAGGGAT GGGAGAAAAG TGGCGACCAC	540
TTGCTGTTT GTTTGCAGTA GCAGGAGTAT TGGTTGCTCT CTTGGGAATC GGAACCTTCA	600
CCCAAGTCAA CTCGATTACA GAATCTATCC AAAATACAAC GACGATTTCG CCAGCCATCA	660
CAG	663

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 727 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CCTTGACCAC CAATTCTTCA CCCGATATGA TGCAGCCCTGC TCGCTGAGCA AGCCCCAAGA	60
GATTACTTAT CTTTGCTTA TTCAAGTCCC AACTCTCTTC TTTTCACCTT GTGATCCACA	120
TAAGCGATCA ACTCGTCATA AAAGCTTCT TCCACTTCCA TGCTAAAGCT GCGGTTAAAG	180
ACCTTCTTCT TTTTCCGCTC TAGGGCTTCT GCATTGTCTA GTTTGATATA AGCGCCCGGG	240

CCATTGGCCT	TGCGGTAGG	ATCAATAAAG	ACTTGTCCCT	CCTTGTCTT	GACAATGCGG	300
AGCAAATCAC	GCTTATCAAT	CACTTCGTTA	GACACAAACAG	ACTTGCGCAA	AGGGATTTTT	360
CTTGTTC	CTTTCCCTC	CTCTAGCAGC	TTTTATTCTT	CTACAGTATC	GT	420
TCCAACTCTA	CTGAAGCAGC	GTCTCCATG	GCTTCAAATT	CGCTAGCAGA	CTTGATATCG	480
ATACGGTAAC	CAGTCAAGTG	AGCCGCCAAG	CGCACGTTT	GTCCACGACG	ACCAATGGCA	540
AGAGAAAGCT	TGTTATCTGG	AACAACCACC	AAGGCACGTT	TGCTGTGTT	TTCATCAAAG	600
ATAACTTGGT	CAACCTCAGC	AGGAGCGATG	GCATTGTAGA	TAAATTCAAGC	TGGATCTGCT	660
ACCCACTCGA	TAACATCGAT	ATTTCTTCG	ATTGGTACCA	TGCGGTCATT	TTTAGCATCG	720
TAACGAG						727

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 563 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

CTAATGTAAA	TCTATGGGAT	AAACGTTAGC	TTCTTTTAAT	AGATTATTAA	GCAATT	60	
AAAACAAC	TC	AAACAA	CTCAACTGGT	TATCTCTGGC	ATATTCAA	GAATACCCAT	120
CTCATCCATC	TTTCAACCA	AGGTTGATGA	GAGTCCACCA	CGCTTGC	GT	180	
AGAGAGGAAT	TCTCCCTCTT	CACGCC	CACCAAGTTGC	TTGGCAACGT	TCTCCCCAG	240	
ACCATCCATT	GCTACAAATG	GTGGGATAAG	GGTATCCCCG	TCGATGAGGA	ACTCTGCGT	300	
CTGACTACAG	TAGAGATCTA	ATTTACCAAA	CTTGAACCT	CGTCCCACA	TCTCATTGAC	360	
AATCTCAAGA	GTTGTATAGA	GATCGATTTC	CACATTAGAG	GCTTCATTGT	TCTCCGTT	420	
TTCAAGAGATT	TCTCCATTC	TGCGCTTGAT	GACCTCCAAG	CCCGCACCCA	TGGTCTTGAT	480	
ATCAAAAGCC	TTAGCACGAA	TGGAGAAAGTA	AGCACAGTAG	TAATAAATAG	GATGGTGAAC	540	
CTTGAAGTAA	GCTACACGCA	AGG				563	

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 647 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

CTAACTTCAA AAGCTTTAG AATATCTTCT TGACTAATCA TATGATTACC GCCCAAGGTT	60
AAGTTTCCA AAATAGAGCC ATTAAAGATA TAGGCTTGT GGGGTAGGTA ATTAATATGA	120
CGGCGCAAGA CTTTTTTAT CAATGTTTT AATATCCTGA TGATTGATGG AAATATGCC	180
TTTGTAGGGT TCAAAGAAAT TGACAATCAT TTTGGCTAAA GTTGGTTTAC CAGAACCACT	240
AACTCCAAC TGGCTAACCT TATCTCCTTG TTTAATCGTG AGATTAATAT CTGTTAAGGT	300
ATCTCGTCCA AAACCATACT TATAAGAAAG GTCATCAAAT TCAATATCGC CCATCAAAAA	360
ATGTGAATGA ACAGGGTTT CTTGAACCTG AAATTCAGAT TCGACTAGAT AGACTTCGTT	420
CAAACGGTTA TTAGCGACCT TCGCAGATTG GAGTTGGTT TGGAGGTTGA TAATATTTTC	480
CATAGGAGTT GTAAAGTAAG AAAGAAGTGT GTTAAAGGTA ATCAGCTGAC CGATAGAAAT	540
TTTACTCGAC ATGACTAATT GAGCGCCAAA CCATAGGATA AGGATATTCA GAACTAATT	600
TGTTTCCCCT GCTTTAAACT CGTTTGTAAA ATAGAATATT TACTGAG	647

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

CTATCCTNGA ACCAATGATG CTTGTAACAA TCACTGTTCC AGAAGAAAAC CTTGGTGATG	60
TTATGGGTCA CGTAACTGCT CGTCGTGGAC GTGTAGATGG TATGGAAGCA CACGGTAACA	120
GCCAAATCGT TCGTGCTTAC GTTCCACTTG CTGAAATGTT CGGTTACGCA ACAGTTCTTC	180
GTTCTGCATC TCAAGGACGT GGTACATTCATCA TGATGGTATT TGACCACTAC GAAGATGTAC	240
CTAAGTCAGT ACAAGAAGAA ATTATTAAGA AAAATAAAGG TGAAGACTAA TCCGTCCTCA	300
CTCTAGAAGG AAGTCACTTA GTGGCTTCCT TTTGTCTTTA GAAAATACCT CTAAATATGG	360
TAAAATAGTA GAAGAATAAT GTGAGGAAAA TGAATGTCAA ATAGTTTGATG AATTTGATG	420
AATCAATTGG GGATGCCTGC TGAAATGAGA CAGGCTCCTG CTTTAGCACA GGCTAATATT	480
GAGCGAGTTG TGGTTCATAA AATTAGTAAG GTATGGGAGT TTCATTTCCG TATTTCTAA	540
TATTTACCTA TTGAAATCCT TTTTACAATT AAAGAAAGTT TGAGCGAAGA ATTTCTNAG	600
AANGCCATCA	610

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 984 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

TATAAGCATA	GTACCAAGTTG	CCATTGACCT	GGAACCAACT	GTCTTCATAT	CTCCATTACT	60
GCATTTAGGT	AGTACCAAGT	TGAACCACCT	TGATACCAAC	CAGTTGCCAT	TGCTCCTGAT	120
GAACGGAGAT	AGTACCAATT	GTTCCAAGG	TTTTGCCAAC	CTGTTTCAT	ATCGCCATT	180
GGCTGGTCTA	AATAATACCA	AGTGGTACCT	TCCTGATACC	AACCAGTTGC	CATTGCTCCT	240
GATGAACGGA	GATAGTACCA	TTTGTCCCCA	AGGTTTGCC	AACCTGTTT	CATATGCCA	300
TTTGGCTGGT	CTAAATAATA	CCAAGTGGTA	CCTTCCTGAT	ACCAGCCAGT	GGCCATTGCT	360
CCTGAGGAAC	GGAGGTAGTA	CCACTTATTA	CCTAGATATT	GCCAACCTGT	TTGCATAATA	420
CCAGTTGTTG	GATCTAAATA	GTACCAAGTC	AAATCATCGT	TTATCCACCC	CGCACGTCTT	480
TCACCACCAA	GGTAGTTTC	TCCATTAATT	TCCGTCTTAG	CTAGATAATA	CCAGTAGACT	540
GATCATAAAG	CCAACCTGTC	TCTAAAGAAT	GATTTTGATT	AAAGTAATAG	TTCGTATAAT	600
AACGNTTCTC	TTCTTTATCT	TCTGAATCTT	CACGTTTTC	CCCGTACTTT	CTTCCAACAC	660
TGTCTTTAGT	TTTAATCTCT	AATGTTTCC	AACCAACAAA	CTCTGTAGC	ACTCCATT	720
TATCGAAGTA	GTACCAACTCT	GAATTTGAA	AACCTTCTAA	TCTCATACCA	TTTGGGTAAG	780
GACCAATTGT	ACTACCTTTA	GATGGAAACG	GGATATATTG	CCAGCCGACA	ACCATCTCTC	840
CAGATAGAGA	ATCAAAATAA	TAGTACTTAC	CATCAATCAC	TCGCCAGTAG	GTTTCTTGAA	900
GGTCCCCCTT	TTTGTAAATAG	GTTCTACCGT	TTTCTGGAC	AAACTGCCAT	CCTTCAGAGT	960
TATCTGCAAA	TACTGTATTC	GTAG				984

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 842 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CCTCGTTATG	CAGATGAACG	TTATTTCTTG	TCAAAGAGTC	ACAAGAATT	TGTTGATCGT	60
AATCTTTTA	TTACCATTCG	TGACAAGGAA	ACCACCTGTA	TCAAGCCTTA	TCAGCAGGAT	120
TTGGATTGTC	CACATGGTCT	GGCCTTGGAT	GTTCGCTT	TGGATTATTA	TCCGAAAAAT	180
CCAGCTGAGC	GGAAAAAACN	GGTCGTTGA	GCCTTGATT	ATTCACTCTT	TTGTGCGCAA	240
ACTATTCCAG	AAAAGCATGG	TGCTCTCATG	AAATGGGGAA	GTCGCATT	ACTGGGTTG	300

ACTCCAAAAT	CTCTCCGTTA	TCGCATCTGG	AAAAAAAGCTG	AGAAAGAAAT	GACTAAGTAT	360
GATTGGCTG	ATTGTGATGG	CATTACAGAA	TTATGCTCAG	GTCCTGGCTA	CATGAGAAC	420
AAGTACCCAA	TCACATCTT	TGAAGACAAT	CTTTCTTGC	CATTTGAAGG	AACAGAGATG	480
CCTATTCCAA	TCGGCTATGA	TGTCTATCTC	AGAACTGCTT	TTGGGGATTA	TATGACGCC	540
CCACCAGCAG	ACAAGCAGGT	ACCGCATTCA	GATGCTGTCA	TCGCTGATAT	GGATAAGTCT	600
TATACAGAAAT	ACAAGGGAGA	ATATGGTGGC	TAAGAAAAAA	ATCTTATTTT	TTATGTGGTC	660
TTTTCTCTT	GGAGGGTGGTG	CAGAGAAGAT	TCTATCAACC	ATTGTTCAA	ATCTGGATCC	720
AGAAAAGTAT	GATATTGATA	TTNTTGAAT	GGAGCACTTT	GACAAGGGAT	ATGAATCTGT	780
TCCAAAGCAT	GTACGCATTT	TAAAATCCCT	TCAAGATTAT	CGCCAAACCA	GATGGATAACG	840
AG						842

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 749 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CTGGCAAATA	CAAGGTGACG	ATCATTGGTA	AATCAGCCCCA	CGGTGCTATG	CCTGCTTCAG	60
GTGTCAATGG	TGCGACTTAC	CTAGCCCTCT	TCCTTAGCCA	GTGGACTTT	GCTGGTCCAG	120
CCAAAGAATA	CCTTGACATC	ACTGGTAAAA	TTCTCTTGAA	CGACCATGAG	GGTAAAGTC	180
TCAAGATTGC	TCATGTGGAT	GAAAAGATGG	GTGCCCTTTC	TATGAATGCA	GGCGTCTTCC	240
GCTTCGATGA	AACAAGTGCT	GATAATACCA	TTGCCCTCAA	CATCCGCTAT	CCAAAAGGAA	300
CAAGTCCAGA	ACAAATCAAG	TCAATCCTTG	AAAACTTGCC	AGTTGTTCT	GTTAGCCTGT	360
CTGAAACACGG	TCACACGCC	CACTATGTTG	CCAATGGAAG	AATCCACTTG	GTTGCAAACC	420
TGGTTGAAAT	GTCTATGAAA	AACAGACAGG	CCTTAAAGGT	CATGAACAAG	TCATCGGTGG	480
TGGAACCTTT	GGTCGCTTGT	TAGAGCGCGG	AGTTGCCTAT	GGTGCTATGT	TCCCAGACTC	540
AATTGATACC	ATGCACCAAG	CCAATGAATT	TATTGCCTTG	GATGATCTCT	TCCGAGCAGC	600
AGCAATTAT	GCCGAAGCTA	TTTACGAATT	GATCAAATAA	AACGATAGAA	GTCTGAGATC	660
TTATGCTTGG	ACTTCTTTT	GGAGGGAAAG	TAGATGTCTC	AAATCGAAAG	AATCAAACAG	720
GCTATCATGG	CGGATTACACA	GAATGCCAG				749

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

CTGGATGAAT TGCAGAAGCG CAACCTACTG GGATTTGTCT TCCAAGATTT TCAACTATTT	60
CCTCATCTAT CAGTTCTGGA AAATTTGACT TTATGCCCTG TGAAGACCAT GGGAAATGAAG	120
CAGGAAGAGG CTGAGAAGAA GGCGAGTGGAA CTCTTGGAAC AGTAGGACT AGGAGGACAC	180
GCAGAGTCCT ATCCTTTCTC ACTATCTGGT GGGCAAAGC AGCGGGTGGC TTTGGCGCGT	240
GCTATGATGA TTGACCCAGA AATCATTGGC TACGATGAAC CAACTTCTGC CCTGGATCCA	300
GAATTACGTT TGGAAGTGGAA GAAGCTAATC TTGCAAAATA GGGAACTTGG GATGACCCAC	360
ATTGTGGTTA CCCATGATTG GCAGTTGGC TGAAAATATC GCACATGTTA TTATTGAAAG	420
TAGAACCTCA AATAGGAAGA AAAATGGATT GAAAAAATGG ATGCTTGTAT TAGTCAGTCT	480
GAAGACTGCC TTTGTTCTTA GTA	503

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

CTGGAGGGCA TTCAGTATTA CTTGAATAGA GGAAAACATC ATCTCCCTTA TGTTCTCAAT	60
ATTGGATTTC CTGGTCAGAA AAATGACCTC TTACTCCTTC GGCTAGATTT AGCTGGAATT	120
TCAATCTCTA CTGGCTCAGC CTGTACTGCA GGC GTTGTCC AATCCAGCCA TGTTCTTAAA	180
GCCATGTATG GCGCAAATTC AGAACGCTTG AAGGAATCCC TT CGC CATCAG TTTGTGCCA	240
CAAAATACCG TTGAAGACCT ACA AACCCCTC GCA AAAACCT TAAAAGAAAT TATCGGAGGT	300
TAGCCATATG GCATTGAAA AAATCATTCA GTAAAAAAT TGCGTTACG ATTACACTCT	360
TAGCCCTTCT GTTAAAAAAT TCACCCCTCAA AGATAACACC TTTTTGAAA CTAAGGTTGG	420
TAACTATGAA CTGACTCGCC TTTTGGAAAA AGTGCCAAAC AGCGGTGAAG GCTTCCAATC	480
CAAAATCATC ATTAACAAGG AAC TTACAGG GGCTAAAATC AATATCACTG ACAAGTTGG	540
CCTTCGTCTA GTTGATATTT TCAAATCAGA AGACCACCAT ATTCA TCAGG AAAAATTCTA	600
CTTCCTCATG GATAG	615

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 954 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

CTGCAATGGT TAGCGAGGAT GGTGAAATAG AGGAGCCTTA ACTATTTGA GGAATCCAAG	60
CTGACAGGAC TGGTATGTCT GCTCTTGTC TCTGAAGGCA GACTATACCA GCTGGAAGTT	120
TGACAGATGT GGCACGTGAG AATTATTGGA GGCNTTGACN TANTCAGAGG ATTCTCTCTT	180
GATATTGGGT TTGGCAGAGT TGGATAGTGA GTTGGAAAAT TACCAAGCGG TTATTCAAGC	240
CTATGCCAG TTAGATAATC GCTCGATTAA TGAGCAAACG GGCATTCCA CCTATCAAACG	300
AATTGGCTTT GCCTATGCTC AGTTAGGGAA ATTTGAAACG GCTACTGAGT TTTTAGAAAA	360
AGCCCTGGAG TTAGAATAACG ATGACTTAAC AGCTTTGAG TTGGCAGTC TTTATTTGA	420
TCAAGAAGAA TATCAAAAAG CCACCCTCTA CTTTAAGCAG CTTGATACCA TTTCTCCTGA	480
CTTTGAAGGC TATGAGTATG GGTACAGTCA GGCTTTACAT AAGGAACATC AAGTTCAAGA	540
AGCCCTGCCT ATCGCTAACG AAGGATTAGA GAAAATCCC TTTGAAACTC GCCTCTTGCT	600
AGCTGCTTCA CAATTTCTT ATGAATTGCA TGATGCTAGT GGTGCAGAAA ATTATCTCCT	660
TACTGCAAAA GAAGACGCTG AGGATACAGA AGAAATCTTG CTTCGTTAG CCACTATTTA	720
TCTGGAGCAG GAGCGTTATG AGGATATTCT AGACTTGCAG AGTGAGGAGC CAGAAAATCT	780
TTTGACCAAG TGGATGATTG CTCGTTCTTA TCAAGAAATG GACGATTTGG ATACTGCTTA	840
TGAGCATTAT CAAGAGTTGA CAGGAGATT GAAGGACAAT CCAGAATTTC TGGAACACTA	900
TATCTATCTC TTGCGTTGAA TTGGGACATT TTGAAGAACG AAAATCCCAT GCTC	954

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 564 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

CTATGAAACA TTTTGATACT ATTGTCATCG GTGGGGGACC TGCTGGTATG ATGGCTACGA	60
TTTCCAGTAG CTTTTATGGA CAGAAAACCC TCCTCATCGA AAAAAATCGG AAACCTGGAA	120
AAAAATTAGC TGGGACTGGT GGGGGACGTT GCAATGTGAC CAACAATGGT AGCTTAGACCA	180
ACCTGCTAGC TGGAAATTCTT GGAAACGGAC GCTTTCTTTA CAGTGTTC TCCCGTTCG	240
ATAATCATGA CATCATCAAC TTTTTACAG AAAATGGTGT TAAACTTAAG GTCGAAGACC	300
ACGGACGCGT CTTTCCAGCC AGTGACAAGT CTCGGACTAT TATCGAAGCT TTGGAAAAGA	360
AAATCACTGA ACTAGGTGGT CAAGTTGCTA CTCCAAATAG AAATCGTTTC TGTTAAAAAA	420
GTAGATGACC AGTTTGTCT TAAGTCAGCG GATCAAACCT TCACTTGTGA GAAACTCATT	480

GTCACAACAG GTGGTAAGTC TTATCCTTCG ACTGGTTCGA CTGGTTTGG TCACAATGCT	540
CCGCCATTAA AGCATACCAT CACG	564

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

CTCCGTGGTC TTTGGTTTG CTACGGGATG TAGGCAAAAG GCAAGTCCAT TTTATCAGCA	60
ATAATGGCTC CGTGTGGAAT CCCTGCTGTT GCAGTTCTG CAATCACTTC TACTTCAGGA	120
AAGGCTTCTT TGATAGCTTC CACAAAACCA TTTTCAATTAA GGTTACGAGT TTCTGGATAG	180
GCTAGTGTCA CACGATTATC AGTGTAAATC GGTGACTTGA TACCAGATGC CCAAGTGAAG	240
GGTTCCCTCTG GTTGAGGTA AACGGCTTGG ATTTTCAAGA GGTGGCTAGC GATATCTTA	300
GCAAGTGTCA TGGTATTCTC CTTTTATTAA TCTAATCTAG TTCTTTAATT CCAGTCCTGT	360
GTCCATTTCAT CCTTGATGGC ATGATAAGCT GCAACAGGAT CCTCAGCTTG GGTAATGGGA	420
CGTCCCACCA CGATATAGTC ACTGCCGATT TGATAGGCAT CAGCAGGTGT CATGACTCGT	480
TTTTGATCTC CAACTGCAAC ACCAGCTGGA CCAATCCCTG GTGCCCCGAC AGATAAAAAT	540
CTGGATTGGT AGCCCTGCTT GATGACTTTG TCACTTCCCT GAGCCGAGCC AAACCAAACAC	600
CCATCCAAA GCCCAAGCTT CAGCTGTCTT CCTTGGCATA GTTGAATCCA C	651

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 602 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

CTTAGTATCT AGAAAAGGAG AAATAAAAATG GTTAAAGTAT TAGCAGCGTG CGGAAATGGA	60
ATGGGTTCAT CAATGGTTAT CAAGATGAAG GTTGAAAATG CTCTCCGTAA GCTTAATCAA	120
ACAGATTAA CAGTCAATTG ATGCAGTGTGTC GGTGAAGCTA AAGTTTAGC AGTAGGATAT	180
GACATCGTAA TCGCTTCTCT TCATTTGATT CAAGAATTGG AAGGGCGAAC TAATGGGAAG	240
TTAATTGGGC TTGATAACTT GATGGATGAT AAAGAAATCA CCGAAAAACT CAGTCAAGCA	300

ATACAGTAAA AGGTTGGAGG GGGCTGGACA CAAACTGAGA GTTATCGTTT CTGTCCTTCT	360
CCCTCTTAA ATAAAGGAGG CAGATATGAA TTTAAAACAA CCTTTAATTG ACAACGACTC	420
GATCCGACTA GGTTTAGAAG CTAACGAATG GAAAGAAGCA GTCAAGGTAG CAGTAGATCC	480
CTTGATTGAA AGTGGGGCAA TTTGCCAGA GTATTACGAT GCTATCATTG AATCGACTGA	540
AGAGTATGGG CCTTACTATA TCTTGATGCC AGGTATGGCT ATGCCAACG CTAGACCTGA	600
AG	602

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 586 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

ATTGGGAATT TTTGCAACTG CAATTGGTGC CCTCAGTAAT CTATAAAATA GATTCAAGAA	60
AATTTAGTGA CTGGGATTTC CCAGCCCTTT TTTAAAGTGA GAAGAAATAA TGAGTATGTT	120
TTTAGATACA GCTAAGATTA AGGTCAAGGC TGGTAATGGT GGCGATGGTA TGGTTGCCTT	180
TCGTCGTGAA AAATATGTCC CTAATGGAGG CCCCTGGGGT GGTGATGGTG GTCGTGGAGG	240
CAATGTGGTC TTCGTTGTAG ACGAAGGACT ACGTACCTTG ATGGATTTC GCTACAATCG	300
TCATTTCAAG GCTGATTCTG GTGAAAAAGG GATGACCAAA GGGATGCATG GTCGTGGTGC	360
TGAGGACCTT AGAGTCGAG TACCACAAGG TACGACTGTT CGTGATGCCGG AGACTGGCAA	420
GGTTTAACA GATTGATTG AACATGGCA AGAATTATC GTTGCCACG GTGGTCCGTG	480
GTGGACGTGG AAATATTCGT TTGCGACAC CAAAAAATCC TGCACCGGAA ATCTCTGAAA	540
ATGGAGAACC AGGTTCAAGGA ACGTGAGTTT ACAATTGGAA CTTAAA	586

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 680 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

TTCGACAATC TTGCCNNGA TCCAAGACAA CCACCTCTCT GTCCGCTCAG CAATAGTCAA	60
GCGGTGAGCA ATGAAAATCA AAGGTCTTGT CCAAAGCCAT GAGATAATGG ACAATCCGTT	120

TTTTTGTCAA AATATCCAAA CTGTTAGTCG CCTCATCCAA AATCAAGACC GGCGCATCTG	180
TCAAGAGAGC ACGCGCCAAA GCGATTCTCT GACGTTGACC ACCTGAAATC CCTGCCCAT	240
CCGAAGTCAA TTCTGTCTGG TAAATTCAA GGTGGCATGG CGGCTTCGAG ATATTCCCT	300
TCGGAATCTC TGAACCAAAT TCGGACCGGC CCGTTAAAGA TATCTCCCT GTGTCGTCCC	360
CTCCCTTGGC TCCCCAAAGA AGATTCTCCA AAATCGTTCC GTTAAAGACA TAGGGCTGTG	420
GAGGCAGATA GATGATGTAC TGGCGTAGGG CTTTTTTATC AATCTGATTG AGATTGACAC	480
CACCCAGACT AATCTCCCT TGACTTGGGT CGTAAAAATT ACCATCATC TTGGCCAAAG	540
TCGTCTTACC TGACCCCTGAA ATCCCCACAA AAGCCACCTT AGACCCCTTGG GGAACGGTTA	600
AATTGATATC CGACAAAGACG TCTCGACCAT AGCCATACTT GTAATGAACC TGCTTGAAAG	660
TCATCTCTCC CTTCATCAAG	680

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

CCAATTGGAA TTTGCGAGAA GGCGTTATTA TTTCAGATGC TGGTCGACC AAGTCAACCA	60
TTGTGGATGC GGCGGAGCAG TATTGCGCTG GCAAGTCTGT TCGCTTGTC GGGGCCATC	120
CCATGGCTGG TAGTCACAAG ACAGGGGCTG CTTCGGCAGA TGTCAATCTT TTTGAAAATG	180
CCTATTATAT CTTTACAACC TTCCAAAGCC CTGAACAAGT CAAGGACAAC GCTTAAAGGA	240
AATGGGAAAG GATCTGCTTT CCAGGCTTTC ATGGCTCGTT TTATCGAGAT TGATGCCAAG	300
GAGCATGATC GTGTCACTTC TCAGATTAGC CATTTCCCTC ATATTTGGC TTCTAGTCTC	360
ATGGAGCAGA CTGCGGTCTA TGCTCAAGAG CATGAGAATG GCAAGGCGCT TTGCGGCAGG	420
TGGTTTCGAA GATATGACCC GAATTGCGGA AAGCGAGCCA GGAATGTGGA CCTCCATTCT	480
CTTGTCCAAT AGCGAGACCA TTCTGGATAG AATTGAGGAT TTCAAGGAAC GTTTGGAAAGC	540
GATTGGTCAG GCCATTAGTA AGGGAGATGA AGAGCAAATT TGGAACCTTT TTAACCAAGC	600
G	601

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

CTGGCTCATC AGGGGCAGGA TATTTATGAT TTCCCTCGTG CTATGATTAA GGAAGATAAT	60
CTGGAGTTTT CATTCTCTGG TTTGAAATCT GCCTTTATCA ATCTTCACCA CAATGCCGAG	120
CAAAAGGGAG AAAGTCTGTC TACAGAGGAT TTGTGTGCTT CCTTCCAAGC AGCTGTACTG	180
GATATTCTCA TGGCAAAAAC CAAGAAGGCT TTGGAGAAAT ATCCTGTTAA AACCCCTGGTT	240
GTGGCAGGTG GTGTGGCAGC CAATAAAGGT CTCAGAGAAC GCCTAGCAGC CGAGGTTACA	300
GATGTCAAGG TCATCATTCC ACCTCTGCGC CTCTGCGGAG ACAATGCAGG TATGATTGCT	360
TATGCCAGTG TCAGCGAGTG GAACAAAGAA AACTTGCAA ACTTGGACCT CAATGCCAAA	420
CCAAGCCTCG CTTTGATAC CATGGAATAA AGAGTGGCTC TTTGTCAAGT GTAGTGGTA	480
GGCGAAAAGC TACAATCTGG AGANTACGAA ATT	514

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

CTTGGATTAT AAAATACAAT CGGCAAGATC ATAAGTCCC AGCCTAAAAA TATATAGAAA	60
GGGGGTCACC TTCCAAAGAA ATTCTGTATT AAAGAGCATG ACCACAAAAC CAATCACAAG	120
CCCCAAGGCA ATCCAGGCGA CCTGCTGCC TAAAATGGGC AGAATATTAT TGGGGTAATC	180
ATGACTAACG GCTATATAGA TAGCCACCA ACCGATGACC AGTAGAAAAA ATACTGGCAA	240
GAGCAAAC TG TAATCGACTC TTGAGTCGAG AGAACGTTTC ATATAAACTA ACCTTATACT	300
TTCATACAAT ACTATTTATC AAAGTTCTATT AAAAATCTA TCAATAGCCT CGTCAACTTC	360
GGATCGAGAG ATGGTTTAA CAGTCGCTTC TTCTGCTAGA GATGCTACTA TTTGTTGCC	420
GTATCGTTT CCGACGATTC TCCTATCCAA AATAAGAGTT AAGGAACGTT GGTATTACG	480
TCTCATACTT CTTCCCAAAG CCTGTTTAA ACGAATAATG G	521

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 599 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

CTTGCGCTGAT GACATCATTG ACTCTTTTG GTATATCATC GACCATTCT TAAAAAAATGT	60
CTTTGAATTG GAAGAAGAAC TCGAGTTCA ATTGCTTAAT AACCAAGGAA AGATTACCTT	120
CCACTTTCA AGTCAACACC TCCCTACAGC CATTGATTGTT GACTTTAACCC ATCCTTCGA	180
CCCTCGTTAT CCCCAAGAG TACTGGTTTT AGACATGGAC GGTAGAGAAA CTATCCTCCT	240
CCCAGAAGAA AATGACCTAT TTTAAAAACT CTAGCCTTCA GTTGCAAGTG ACTGAAA	300
AGAGTTTTTC TATTTTTCA AAGCATCATA CAAGTTGCCG ATCGGTTGTT TTAATATCGG	360
ATGGATAAAA TGAGGCGCAA TTTCCTGTAA GGACTCAAGG ACAAAAAGGC GTTCCCGCTA	420
TGTAAAGGGA TGAGGCAATA TGAGTCGTC TGTATAAAGG ATCTGGTCCT CCCACAAAGA	480
GCAAGTCCA AATCAATCCA AACGAAGTCC CCCAATGCAC TTCTCTCACC CGTCCCCAGC	540
TCTTGACTCC AATGGCTAAC AAGGTTTCNT ACAATTCTT GTTGCTGGTA GCCAAGTTC	599

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

CTATGGGTAA AAAGGATGCC TCTGCTATGC ATGAGATGAG GGCTTCCTTT ATTCAAGGCT	60
CCATAGAACG AGGCCACT GCAGGAAAAT CAGAGCAGGT TTTTGATGTT ATGGAGAAGT	120
TTGCAGGTAA TCGATTTAAT AGATCTCATG CCTACGCCTA CTCAGCCTTG GCCTTCCAGT	180
TGGCTTATTG CAAAACGCAT TATCCAGCCA TTTTTTATCA GGTCATGTTA AATTATTCCA	240
ACAGTGATTA CTTAATAGAT GCACTTGAAG CAGGTTTTGA AGTAGCCTCT CTATCCATCA	300
ATACTATTCC CTATCACGAT AAAATTGCCA ACAAGTCTAT CTATATAGGT TTGAAATCGA	360
TTAAGGGCT CCAGCAAGGA CTTGGCGCTT TGGATTATTG AACATAGACC TTATTCTAAC	420
ATTGAAGATT TTATAGCTAA ATTACCTGAG AATTATCTGA AACTTCTCC TGCTAGAAC	480
TTTGGTAAAA GTTGGTCTTT TCGATTCTATT TGAAAAAAAT CGTCAAAAG TATTTAATAA	540
CTTAGCTATC TATTGAATTG TGAA	564

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

ACTAATCACT TACTACGTAG CTTCTGACTA TCTACCTCTA CTAGATAAAAG GACAAACTGT	60
AAGATTAAAA CTGGAGAAGN TTGGAAATCA CGGCATTACC ACCATCGGCC AACTTCAGAC	120
AATTGATCAA ACTCCTACCA GAACAGAGCA AGGCAATCTC TTTAAATTAA CCGCTCTTGC	180
AAAACATATCT AATGAGGATA GTAAACTCAT CCAATATGGC TTACAAGGTC GCGTCACTAG	240
TGTAACTGCA AAGAAAACAT ATTTTGATTA TTTCAAAGAT AAAATTAA CCCATTCTGA	300
TTAATTTCA GATAACACTC TATAACTATT TATTATCTTA TCAAAAAGGA GAATCATAAC	360
ATGGATAAGA AACAAAACCT AACTTCATTT CAAGAACTAA CAACTACCGA ACTCAACCAA	420
ATTACAGGTG GAGAATGGTG GGAAGAACTC TTACATGAAA CAATTAAAG TAAATTAA	480
ATCACAAAAG CACTGAACT ACCTATTCACT CTATAAAAAC AAGACCGAGA AACAGAACT	540
CTCGGTCTTG TTTTTTATCA TTCTGCATGT ATCACAGTAA GTACCTGACG AAAGACTTGA	600
TTTTGGCGAG GTAGTATT	618

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CAGGGGATGC CAGTTGATTT GCTTCAAGTT GACTTGACTC GTACTTGGGA AATCCTCGGA	60
GAAATCACTG GGGATGCTGC TCCAGATGAA CTCATCACCC AACTCTTTAG CCAATTCTGT	120
TTAGGAAAAT AAGAAAATC CATGATCCTT CATTGGTCA TGGATTTAT TGTCTTTATT	180
AGTAATCTGG TCTTAAGACC CCTGTTACAG TTGCCTTAGT TGCTTCGTAG TCGCCATCTA	240
CGACAACCTT GATAATGCGT TTGACATCTT CTTCTGGTGC TGGAACAAAGA GGTAGACGAG	300
TGGGTCCAGC TTCAAATCCC ATATAGTTAA GAATTGCCTT AACTGGAGCA GGACTTGGAT	360
AAGAGAAAGAG AGCATTAAACC TTAGGAATGA ATTACGCTG AATTGCTGCG GCTTTCTTCA	420
TATCGCTTTC TGCAATGGCA GTAAACATCT CGTGCATTTC ATCCCCATTT GTATGAGAAG	480
CAACAGAAAT AACCCATCCG CCCCCAAGGTT CATGGCATGG AAAGCATCTC CATCCTCAC	540
TGTATAAAT	549

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

CTGGCTANCA AAATCATACT CATAATCCTT AACACCGACA GAGATAGAAG CAATGAGCCC	60
TTGATCGTGC ATTCGTTAA TAAAAGGAAT GCGTCCTGCC TCATCAAAAC GGTGCATAAG	120
TGTACAAGTA ACCACCTTTA GCCAGTTGCT CTGCTACATT TTCATCCAAA ATCGTCTGCA	180
TATTCGCTGG CACAAACAGGT AGTTTAAAGG TGTGATTCC TAAAGTGACA CTTGTATCCG	240
CTTCTGCACG GCTTTAATG ACACATTAT TTGGAATCAA TTGAATATCT TCGTAATCAA	300
AAATTGGAAA TTCATTTAAC ATATCGATGT CTCGTTCTT TTGTAATGAC CTACCTATGC	360
TCTCGCATCA CTACGCCCTT TCCGACGTTT CCCTTAAATT TATTATAAAC CAAAAGTACA	420
GTTTTGTCA AATTATTTCA TGAATNAAAT ATATC	455

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 776 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

CTCCTGGGTT TTGATTAACT CTAGGGTTGC CAAAAAGAGG GTGATGACTT CTTGGACATT	" 60
CTGGGTTCC TTGAACAAAT CCTGCAAGCG CAATTGATT CGTCCAATCA AGGATTCTTT	120
CACAATAATC ATCATGTCCT CAATCTTATA CTCATCCCGC AAGATAGTCG TGTGATTGG	180
TGCAAACCTCC TCTTTTTCT TGGCTAGGAT ATTTGAAAAA GCCAAAAAGA GGTCAATGGT	240
CGTCTTGTCA TGCACAAGCT CCGCATCTTC GTAAATCAAC TCTATGGCG CTTTGGAAATA	300
ATACTGGGCC CGTTTCTTGG TGCTTGGCTT CCAAGTGCTC ACCCAAGAGC TTGAACTTGC	360
GATATTCTTC GATTTGAGAG AGGAGGTCCT GCTCCAGGTC ATCCCCCAAG TCTGTCACCT	420
CTGCTACCTT CGGAAGGAGT TTACGACTCT TAATCAGCAT GAGCTGACTA GCCATGACCA	480
TGTACTCACC CGTCACCTCC AGACGCATGG CCTGCAGGGT TGAGACATAG GCTAGATACT	540
GTTCGATGAC TTCCGTAATG GGCACATCGT AGATATCCAT CTGGTACTTA GAAACCAGAT	600
GCAAGAGTAA GTCCAGGGGT CCTTCAAAAT CTTTTAATT AATATCCATT ATCTATATT	660
TTCTAAGGTC AGGACTGTTT TTAATCCTAA TTTTTTGCA ATTCGTACA AATCGACCTT	720
GTTTCTATT TGTCCCTAGA ATAAACTGTT CACGTAAGAC TTGAGATCGA ATTCCCT	776

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

ATTGATACCN ATTGTACAGG ACAACTTATT TTGGAGCGCC ATAGCAGGGA TANGTTAGC	60
AATAGATGCG NTGACCATAG AAACGTTNT TAGCCAATAC ATAACCTGCT AGAGATGAGG	120
TTGCACAAAC TAAGAACATG GTTACCAATG AGATAAATAC TGAGTCCAC ATCCATIGCA	180
AGGCAGGGTT CTGCACCATG AGTTGTTGGA AGTTTTCCAT GGTTGGCATT TTAGGGAACC	240
ACTGAGGAGG AATAACAATT GTATCAGGTT GTGATTTGAA TGCCCCCTGTC AAAATCCAGT	300
AGAAATGGAAA GATGNACAGC ACAGTCAACA AGAGCAAAT GATTGTTGAA ATNACAGTAA	360
AGGCTGTTAA TGGTTTTTT TCTGTAGATT GCATAGCTGT CTCCTTTCTT TAGTATTCTA	420
CGTCGTTCC AAGTACTTTA AATTGAACAA AGCTTACGAT AGCAATCATG ACTGCCAAGA	480
AGACACCAAT TGTGTTGGCA TAGCCGTATT CTGTCAATTG GAAGGCTTT TCGTAAAGGT	540
AGTACATCAA GGTACTTGTT GAGTAGTTG GACCACCAGA TGTAAAAGC TGAATCAAGG	600
CGAAACACTG GAATGAGTTA ATTGTTGTGA TGATTGCAAT ATAAAGAGTT GTTGGAAAGAA	660
GGCTTGGCCA TTTAATCTTC CAAAAAACTT GAAACTCAGT TGCACCACATCA ACACG	715

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

CTGGGCTGAG TTTTCCAGAT ACAAAACTG CAACCGAAC TGCAATCCCC CAACCCATAG	60
TAATCACAAT CCAACCTGCA CTGTTGCTCT TGGTTTTGGA AAGAACCAACA CCTGCAACAA	120
CACCATTTCC TAGAAGAACAT AGGATTAAAG TCCCTAAAAA TTCTCCAAAT AATTCACTCA	180
TCATTTTCT GTCTCCATTA AAAAGAAGGG CGGGCGACA AGGATTGCTA CCCTCCACCT	240
CTTTTATTT TTCTTAATT TTTAATTCTG CTAAGTCGTT TTGAGCAAGA GCTGTTTTA	300
CATCAGCAGC GTAAGTTGCT TTTTCTTCTT CTGTCCAGTC ATAGAATCGT CCCATTTCAT	360
CCAAAAACTGG CTCAACGATA CTATCCAAGC TATCACGCAT AAAGAGCATG TGATTGGTAC	420
GACGAAGAAG GAAGTCAACT GGGCTAAGAG TCAACTCATT GCGCATTGCA TAGTGAAGGG	480

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 670 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

CTTAATTATA	ACTTAAACAC	AAAAGTTTA	CACAAACTGT	GGATAACTCT	TTTGAAACTG	60
TGATTTCTT	AATTGAAATC	TATTTTTAT	TTTGTGAATA	AGATGTGAAA	AAATAGAGAA	120
TATGTTAGAA	TAGAGTCATG	AAAATAAAG	TTGTAACAGT	TGGAAACTG	AAAGAAAAGT	180
ATTTAAAAGA	TGGTATCGCA	GAGTATTCAA	AACGAATTTC	TAGATTGCT	AAGTTGAAA	240
TGATTGAGTT	ATCAGATGAA	AAAACACCAAG	ATAAGGCCAG	TGAATCAGAA	AATCAAAAGA	300
TTTTAGAAAT	AGAAGGTCAG	AGAATTAT	CAAAAATTGC	TGACCGTGAT	TTCGTTATTG	360
TGTTAGCCAT	TGAAGGGAAA	ACTTTCTTCT	CAGAAGAATT	TAGTAAGCAG	TTAGAAGAAA	420
CTTCTATAAA	AGGANTTTCT	ACTCTTACTT	TTATTATTGG	GGGAAGTTA	GGATTGTCAT	480
CATCTGTAAA	AAATAGAGCC	AATCTTCTG	TCAGTTTG	TCGCCTAAC	TTGCCTCATC	540
AGTTAATGAG	ACTAGTTCTT	GTTGAACAAA	TCTATCGCGC	TTTACGATT	CAGCAGGGAT	600
TCCCCCTACCA	TAAATAGAGA	ATTGACTTT	AATTGAATT	TTGGTAGAAT	AATTGTGTTA	660
GGTCTCATAG						670

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

CTATAATTAA	ATTAGCTGTA	TTCCAGTCGT	CACGACCAAA	CTCTGTTACA	GGGACACGAA	60
TGTCAAAACG	GTTCTCAATC	TCCACAATCA	ACTCAACCGT	TCCCATACTA	TCCAAGACAC	120
CTGCATCAAA	AAGATTTCA	TCCATCATGT	CAGAAACATC	TTCCATAAAC	AACTCATCAA	180
TAATTTCGAT	AACTTCTGAT	TTGATATCCA	TATTTTATT	CCTTTTATT	TTTAAACCAT	240
AGATTATTCA	AGAATCCAGA	AAAGATTAAG	AATGACAACA	TGACAACATG	GAAAGTGACA	300

ACCATGCCAA GCAACTGAAT CCAGCGATT TCAGGTAGGG CAGCCTTCCC TGCTTTTTC	360
CGTTCCCTTAT TGAGCGTTTT TTTCTTGCAG ACCCAGGCAT CATTGATGAA CAAGCCTAAG	420
TCCATGAAAG AGTCCCCATAG GCGATATAGT ACCAGGTAC ACCATGCCAA AATCCCCATA	480
ATCCAGCATA TTTACAATGT AAGATC	506

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 921 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ATGGTTCGAC CCACAAATAT GTTTTGCAGA TCATTGACCA TTCTATGATT TACGTTGCCA	60
TTGCCGGCTC ATACACGCC CTTGTCTTGA CCTTGATGAA TAACTGGTTT GGCTATCTGA	120
TTATTGTCAT CCAATGGGA ACGACCACCT TTGGTATTCT CTATAAAATC TTTGCTAAA	180
AGGTCAATGA GAAATTAGC CTTGCTCTT ACCTGATTAT GGGCTGGTTG GTTCTGGCTA	240
TCATTCCCTGC CATTATCAGT CAAACNACAC CCGTTTCTG GATTCTCATG GTAACTGGCG	300
GACTCTGTTA TACAGTTGGA GCTGATTGAT AGCCTTTATG CATTGAAATT TGACAGTTG	360
ACTTATGAAA ATAAAGCAGA GGTTATGGAC TTTATCAAGG CTCGTGTTGA TAAGATGATG	420
GGCTCTACTC CAAAAGATAT CAAGGGAAAGC AGTCTTGCA GGTCAAACACT TTGTTGTGGC	480
AGATATGTTT GGAAGCAGCA AGTGCTCTG TAGAAGTAAG CAAGGAAGAA GATTTAAC	540
CATCTGTTGA ATCACTTTCT CGTGCCTTA ACCTGGCTGA GAAGGCAGAA GGGGTTGCTA	600
CAGTTGATTC AGCACTATTT GAGAATGACC AAGAAAAAGC TTTGGCAGAA GCAGTAGAAA	660
CACTCGTTTT ATCAGGACCT GCAAGTCAGC ATTGAAACA ACTCTTGCG CTTAGCCCAG	720
TCATTGATGC TTTCTTGAA AATACTATGG TAATGGCTGA AGATCAGGCT GTCCGTAAA	780
ATCGTTGGC AATCTGTCA CAACTAACCA AGAAAGCAGC TAAGTTGCT TGTTTAACC	840
AAATTAACAC TAAATAAAAT TTGATAAACG GACTTTATCT TATTACAAAG GAGAAGAAAT	900
GGATCCGAAN ANATTGCTCG T	921

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 571 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

CTTGGCAACA GGCTCTTTT GTATTGCGTT TATTAAGAAA AACAAAAAAC ATCGATATAA	60
CATTTAACTA AAAATTATTG TATGTTATCT CCCTTAATTA GGAATGATAA GGGAAATAACT	120
AGAAAGATTT GTGAATACAA ACTATTCTG ATATACAAAA TATACAGTAA TAATGAATGA	180
TGGGAGATGG GATGAAAGAA TTTCAATTG AGAGAAAGCA GCGTTTTCT TTGAGGCCAT	240
ATGCAATAGG AGCTTGTCG GTCTGCTAG GAACGAGTT ATTTTTGCT GGTATGGTG	300
CTCAGCCTGT ACAGGATACA GAAACGAGTT CAGCACTAAT TTCAAGTCAT TATTTGGATG	360
AGCAGGATTT ATCTGAAAAG CTGAAATCTG AGTGCAATG GTTGAAATTA GAAAACAAGC	420
TTTTGAACCTT ATGGGAACAT TAGGTTACTA TGAAGGATTT GTTCCCTTATG TTTCAAATCA	480
ATACAAAAAC CAAGCTGAAG AAGAAGCAA ACCGCTATCT GATAAAATATA TTTCGAAAAA	540
ATCTTAAGAA AAACATATGC ACCTTCAAAAA A	571

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 611 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

GTATCAACTC CAAAGAGCAA GTGACTGTCA AAGTTGTAAC AGATGCGGCC AAGAAGCTCA	60
TGGGTGATAA GATTGCTCGC CAGAAAGAAC GTGGGATTCA GATTGANACC TTGCGNACCA	120
TGATTATMGG GATTCCANAC GNTGGTAAAT CCACTCTGAT GAACCGTTG GCTGGTAAAA	180
AGATTGCTGT TGTTGGAAAC AAGCCAGGG TCACAAAAGG TCAACAATGG CTTAAAACCA	240
ATAAAAGATCT GGAAATACTT GGATACACCG GGGATTCTCT GCCCTATAGT TTGAGGATGA	300
AACTGTTGCA CTTAAGTTGG CATTGACTGG AGCTATCAAG GATCAGTTGC TTCCTATGGA	360
TGAGGTTACC ATTTTGTTA TCAATTATTT CAAAGAACAT TATCCAGAAA AGCTGGCTGA	420
ACGCTTCAAA CAAATGAAAAA TTGAAGAAGA AGCCCTGTG ATTATTATGG ATATGACCCG	480
CGCCCTCGGT TTCCGTGATG ACTATGACCG TTTTTACAGT CTCTCCGTG AAGGAAGTCC	540
GTGATGGCAG ACTCGGTAAC TATAACCTTAG ATACATTGGA AGACCTCGAT GGCNACGATT	600
GAACTAAGTC C	611

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1054 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

TTGCTAAAGC AGCCATGATG ANGGCACTCC ATAAGGATAA GTACCACCAA GCAGCAGCAG	60
ANGACCATAA TCTCCTTAT GACTTGAACG AGAACGTTCA ATAATAACTT TTTCTAGTAA	120
GGTTTGATTA ATCACTTCA TCCTTTTCC CTCTCACTT TATTATACAA CAAAAAGGAG	180
ACGCAGACCT CCTTTGTAA TCTTATATCT AAAATTTAAT ATTCAATTCT GCCATTTAG	240
ATATAGCTAT AGAAAATACA CTCTATTAAT CGAATGTTTC TCTTATTTTC TATCCAATGT	300
CCGAAGTGT GCTTGATAAG TTTGCTCCAT CAGCATGGTA ATGGTCATAG GACCGACACC	360
TCCAGGGACT GGCGTGATAT GGCTAGCAAG TGGTGCAACT GCCTCATAAT CAACATCTCC	420
ACAGAGCTTC CCATTTCAT CTCGGTTCAT CCCAACGTCA ATGACAACCG CACCTGGTTT	480
GACAAAGTCA GCAGTCACAA ACTTGGCGCG GCCGATTGCC ACTACAAGAA TATCTGCTTT	540
AGCAGCCACC TTGGCAAGAT TATGAGTTCG TGAGTGGGCC AAGGTTACTG TCGCATTTC	600
AGCCAAAAGA AGCTGAGCCA TAGGTTTCC AACGATATTT GAACGACCGA TTACGACCGC	660
ATTTTACCT TCCAAGTCAA TCCCATATTC ATGAAACATT TCCATAATTC CTGCAGGTGT	720
CGAGGGAATC ATGACTGGAT GTCCAGACCA AAGACGTCCC ATGTTTAGGG GATGGAAACC	780
ATCCACATCC TTTCTGGGT CAATGGCTAA TAAAACCGCC TCTTCATCGA TATGTTTGG	840
TAATGGCAAC TGGACCAAAA TCCCATGCCA AGCTGGATCC CTGATTATAT TTAGCAATCA	900
GGTCTAACAA TTCCCTCTGA GTTAATGGTC TCTGGAACTC GCACTACTTC GCTACGGAA	960
CCAGCCGCAA GAGCTGACCT CTCCCTGTTG CGAACGTTAA ACTTGGCTGG CTGGATTATC	1020
CCCAACCAAA ATCACTACCA ACCAGGCACT AGAG	1054

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 598 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

CTGAACTGGA TTTTGCTACA AGGTCTGATT TGTCAAAGAG ATGCGAGTTA TGATATGAAG	60
CAGGATGATT TGGATAAGGT AGCAGATTAT CTCTCAAAA CAGAAGAATG GACCATGTAT	120
GAGTTGATTC TTTTCGGTAA CCTCTATAGT TTCTACGATG TAGACTATGT CACTCGGATT	180
GGTAGAGAAG TTATGGAGAG GGAGGAATT TACCAAGAGA TTAGTCGCCA TAAGAGATTA	240
GTGTTGATTG TGGCCCTCAA TTGTTACAG CATTGTTAG AGCATTCTTC TTTTATAAT	300
GCCAACATT TTGAGGCTTA TACAGAGAAG ATTATTGACA AAGGTATTAA GCTTTATGAG	360
CGTAATGTTT TCCATTATTT AAAAGGTTT GCCTTATATC AAAAAGGACA GTGTAAAGAA	420
GGCTGTAAGC AGATGCAAGA GACCATGCAT ATTTTGATG TGTTAGGTCT TCCAGAGCAA	480

GTTAGCCTAT TATCAGGAAC ACTACGAAAA ATTTGTCAA AGTTAATTTC CCCAAATAAG	540
GGAAAAAATA AAAAGCTCCT TTGGGTTTG ATACAATAGT TTCAAAATTT GAGAGGAG	598

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

CTACTTCCCG GCCGAGTCGA TTCTCCGCCG ATATCGAGCA TACTGGCTCC TTCTGTTATC	60
AATTTACGAG CCTGCTGGAG CGCCTGCTCA AGAGCAAAA ATTGACCACC GTCCGAAAAG	120
GAGTCTGGGG TTACATTGAT AATTCCGCAA ATAGCTGTCT TTGCATGAGT GGCTTTACTG	180
GACATATCGG TCACTCCCTC AAGGCTATTTC ATCATATTAT TTCTCTATTT TACCATAAAA	240
AGAAAAAGAT GGACACGATT TCATTCATCT TTCTCCCAGT AGAAACAAAGT AAGCAATTGT	300
CAATAATCTT AAACAGAAAT CCCTAATGTC CGACTCATAA TCACCACAAG AGCCAACAAA	360
CAGAAAGCAA TCCCATTAAAC AATCATGTGA AGTAAGATCG ACATTTCCAA ACGTTGGTC	420
TTGTAGGCTG TCCAAGATAG AACTGTCGAC ATACCTCCAT AAATCAATAA AGAAGGTAAA	480
TTACTTGGTT GATGTAATAA AGCAAACACA ATCGTACCGA CTACAAAT	528

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

CTATGAGAGA GAATGACCTT CTCTTGATTA CTGGGGACCA TGGAAATGAC CCAACGTATG	60
CAGGAACGGA TCACACTCGG GAATATATTC CATTGTTGGC CTATAGCCCT GCCTTTAAAG	120
GAAATGGTCT CATTCCAGTA GGACATTTC CAGATATTTC AGCGACTGTT GCCGATAACT	180
TTGGTGTGGA AACTGCTATG ATTGGGGAAA GTTCTTAGA TAAATTGGTA TAAGATGACG	240
CGCTATGCTT TGCTGGTGAG AGGTATCAAT GTTGGTGGTA AGAATAAGGT CGTCATGGCG	300
GAGCTTCGTC AAGAATTGAC AAACCTGGGA CTGGAAAAAG GTTGAGAGCT ACATCAATAG	360
TGGCAATATT TTCCTTACT TCGATAGATT CCAAAGCCCC AATTGGTTGA AAAAGCTAGA	420

GACTTTCTTT GCAGTCCATT ATCCATTTAT TCCAGAACTT TTTCCTTAC TGAGTCTAGA	480
GGACTTTGAA GGGCGGAACT TGAAA	505

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 876 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

CTATTTCTC ATCTTTTTA GACTGGTAAT GTATCCCCTA GAGTTTCATT GTTAAGACCT	60
GTCGTATTGA CAACAGTGG A TCCTGATTCC CCATTCCAAG AGTTTGCCC GCATCATATN	120
GACGAAATCT TTTTCTGAGC CAGCAATTTC CTCAGCTAGG GCAATAGCGG CGCTGTTGGC	180
ACTAGATACC AGAGTTGCTT CAAGCAACTC TTGACAGTA TAATTACGGG CCTCCATAGG	240
AATATTACTG GCTTCAGAAT TTGTCGTCAA TTGATAAGGA TAATCAGAAA TATCTACAGG	300
AGTGGAGAGG GTAATACTTC CGTTTCCAA AGCTTCATAG ACCAGATAAA CAGTAATCAA	360
TTTTGTTATG GAAGCAATT CGACAGGTGG CGTTGCATCC TTCTCATAGA GAATTTTACC	420
AGTATTTGCC TCAACAGCAA TCGCATGTT AGCGGCAATG GTAAAATCTT GAGAACAGC	480
AGTAGAAAGCA CCCCCCTAAAAA GAGAGACAGT TAACAAAGTT AAAAATATTT TTTTCATAGT	540
AGTCTTATTC TATCATAAAAG AAAAAAAATA TTCTTGCTTT AATAATTCTAT CTGTTAAGCT	600
TTTTGAAAAT ATGGTAAAAT AAAGTGAGGG AGGTAACTCA TGTTTCTAG AAATAAATTAA	660
TTTTTTGGA CCACAGAAAT TTTACTCTTA ACCATCATCT TTTACCTATG GAGACAGATG	720
GGGTCTTGTGA TTAACCCTTT TGTTAGCGTG CTTAATACAA TTATGATTCC ATTTTTATTA	780
GGGGGCTTTC TTTATTATTT GACAAACCTT ATTGTTACTT TCTTAAATAA AGTCTGTAAA	840
CTCAATCGTT TGCTTGGTAT TTTAATTACC TTGTGT	876

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

CTTGTCAAAT GCCATGGAAG GGGTTCTTTA CTTCTCTAAA CCAGACTTTT CAAAAGTGAC	60
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TAGCGCTGAT	CTCCTCTATG	CTCTGGGACA	ATCTTCTTT	GCCCTCTCAC	TAGGGGTTAC	120
AGACATGTTG	ACCTATGCTT	CTTACTTGGGA	CAAGAAAACC	AATCTAGTC	AGTCAGGAAT	180
CTCCATCGTA	ACCATGAATA	TCTCGATAGT	CCATCATGGA	AGGTCTAGCC	ATTTTCCCAG	240
CCATGTCAGC	CTTCAATATC	CACTCTGAAA	GGGGACCCAG	CCTGCTCTTT	ATCGTCTTGC	300
CTCAACTCTT	TGACAAGATG	CCTTTTGGAA	CCATTGCTA	CGTCCTCTTC	CTCTTTGCAA	360
CTGTCACCTC	TTCTGTCGGT	GATGCTGGAG	ATCAATGTGG	GCAATGTCAC	CAACCAGGAT	420
AACAGCAAAC	GTGCCAAATG	GAGTGTATT	TTAGGAATT	TGACCTTTGT	CTTTGGCATT	480
CCTTCAGCCC	TATCTTACGG	TGTCATGGCG	GATGTTACAC	T		521

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

CTGCAGACAA	TAACTTGGTT	AGCTTAACGG	CTCTTGAGGA	TTCATCCAAG	GATGTAACCT	60
TTACCAGTTC	GGCTTCAAT	CTAAAAGAAC	GGCGACACCT	TCAAAAGGG	GATTCCAAGA	120
AAATCCTTAT	CCACGAAGAA	TTGGCTAAGA	AGAACGGTCT	TTCACTTCAT	GACAAGATTG	180
GCTTGGATGC	TGGTCAGTCT	GAATCTGGAA	AAGGACAAAC	AGTAGAGTTT	GAGATTATCG	240
GCATCTTCC	TGGTAAAAAA	CAAGAGAAAT	TCACAGGCTT	GTCTTCTGAC	TTCAGTGAAA	300
ATCAAGTCTT	TACAGATTAT	GAAAGTAGCC	AAACCCTTTT	GGGCAATAGT	GAAGCTCAAG	360
TCAGTGCAGC	ACGCTTCTAT	GTTAGAAAAT	CCTAAGGAAA	TGGACGGACT	CATGAAGCAG	420
GTAGAAAATC	TGGCCTTGGA	AAATCAAGGC	TACCAAGTCG	AAAAGGAAAA	CAAGGCTTT	480
GAACAAATCA	AAGACTCAGT	TGCAACTTTC	CAAACCTTCC	TGACCATCTT	CCTTTATGGA	540
TGTTGATAGC	AGA					553

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

CTATGGATGC GGAAGTTCT AAGAACCTTC GCTTGATCCT TGAGCGTAAA GGAATGACCA	60
TCTTGACTGG TACTAAACTG CAAGAAATCA TTGAGGAAAA TGGTCAACTT CGTATCAAGG	120
TTGAAGGAAA AGACAATATC ATCGCAAGCA AAGCTTTCT TTCAATTGGT CGTATGCCAG	180
ACCTTGAGG TATTGGAGAG GTTGAGTTG AATTGGATCG TGGTTGTATC AAGGTCAATG	240
AATACATGGA AACTTCAGTT CCACGCATTT ATGCCACCAG GTGACATCAA CGGTACTAAG	300
ATGTTGGCTC ACGCAGCTT CCGCATGGT GAAGTTCCG CTGAAAATGC CCTTAAAGGA	360
AATCATGCAG TTGCCAAATT GAATTGACT CCTGCAGCCA TCTACACTCT CCCTGAAGTA	420
GCAGCAGTAG GTTTGACAGA AGAACAAAGCC CGTGAGAAAT ACGATGTTGC CATCGGTAAG	480
TTTAACTTG CTGCTAACGG TCGTGCTATT GCATCTGACG CAG	523

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 508 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

CTGCAGGTGG AATTATGAAT GTCGGATATG AAAAAGCATT CTTGATGCAG ACATCGTTAA	60
ATTTGCCAAC TTCTGAAATT ATCTCGACAT ATGTCATAA AGTTGGTCTT GTATCAGGAG	120
ACTATTCTTA CTCAACAGCG GTTGGTTGT TTAATGCAGT GATTAACGTA GTATTGCTTG	180
TTGCAGTTAA CCAAATCGTT AAACGCATGA ATAATGGTGA AGGAATTAA GGAGGAAAGT	240
ATGAAAAAATT CGATTATGGA TACAAAATTT GATAGACGTA TCTTACTCTT AAATAAAATC	300
ATTATTGTCT TTATCGTTT GATGACTTTG CTTCCCTTAC TTTATATCGT CGTAGCATCC	360
TTTATGGATC CTAAGGTTCT GGTTAGTAGA GGGATTAGCT TTAATCCAGC CGATTGGACT	420
GTAGAAGGTT ACCAGCGTGT TATTCAGTGA CCAATCTATT CTAAGAAGTT TTATCAATT	480
CCTACTATAC TCTTTGGAT TTGCAGCT	508

(2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 528 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

CTAAAAAGAA CCAGATGGAT CTTGTGATGA ATTTACATCA TTTTGATTCA CCAGTGGAAC	60
TTCTTCAAAA ATACGGTGGT TGGGAAAGCA AACATGTAATG GGAGTTATTG GTGAAGTTG	120
CCAAGACTGC TTTCAACATG CTTTGGAGAT AAGGTTTCATT ACTGGACAAC TTTCAATGAG	180
CCAATGGTCA TTCCAGAAGC AGGATACTTA TATGCTTCC ATTATCCAAA TCTAAAAGGA	240
AAGGGAAAAG AGGCCGTACA AGTCATCTAT AATCTAAACC TTGCTAGTGC AAAAGTGATT	300
CAACTATATC GCTCATTAGG ACTTGATGGA AAGATTGGGA TTATTTTAAA CTTGACACCT	360
GCTTATCCAA GAAGTAATTG TCCAGAAGAC TTAGAAGCAA GTCGATTTAC AGATGACTTC	420
TTTAACAAAG TCTTCCTTGA ATCCAGCTGT TAAAGGAAC TTCCCAGAAA AGATTGGTAA	480
AAACAGCTAG AGAGAGATGG CGTGTATGG AGTCATACCG AAAAAGAG	528

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 778 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

ACTCTTATTG GTGAGGTATC GCAACTTCTG TTTCTGCCCT CCTTGGTGGA CCAGCCAATA	60
CAACTTACGG AGAAAATACA GGGGTTATCG GTATGACTCG TATCGCTTCT GTCTCAGTTA	120
TCCGTAACGC TGCCTTCATC GCGATTGCCG TCAGCTTCCCT TGGTAAATTC ACTGCCTTGA	180
TTTCAACTAT TCCAAACGCT GTACTTGGTG GTATGTCAAT CCTTCTCTAT GGGGTTATCG	240
CCAGCAATGG TTTGAAAGTC TTGATTAAG AACGTGTGGA TTTCGCTCAA ATGCGAAACC	300
TCATCATCGC AAGTGCTATG TTGGTTCTTG GACTTGGGAG GAGCTATCCT TAAACTTGGT	360
CCAGTTACAC TTTCAGGTAC TGCCCTTCA CCCATGACAG GAATCATCTT GAACTTGATC	420
TTGCCATAAG AAAATAAAGA CTAAGAGTCT AAATACACCT AATCCACTCA GACAGCTGAG	480
TGGATTTTC GTATACCATA ATAAAAGTGT CTTAACAAAA TTATTTAAAT CAAAAAAACGT	540
ATAATATCAG ATATTCTAAA ACCTTGATAC TGTACGTTT ATCATAGAAA TTTTTACTTT	600
ATTTTCTCAT CAAATGAGAT TTGCATCAAT CTCTTGTCTT ACTTGCCTTT CTTCTTCGCT	660
TTCTTCATTT TGTTAGCCAT ACGTTTCATG GACTGTTCA TGGCAAATTC ACCAATTAA	720
CCTTTCAAAC CGCCACCAAA CATCTGGCTC ATATCTGGCA TTCCTGCTCC TCCGAGAG	778

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 622 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

GGGAGTTGGT	TGCTATTNGT	GAGGGAAAAG	GTTGAACTT	TGAAATCGAA	GTGGATGGTG	60
GGATTGATGA	CCAAACTATT	GCTCAAGCCA	AAGAAGCTGG	TGCGACTGTT	TTTGTAGCAG	120
GTTCCTATGT	CTTTAAGGGA	GAAGTCAATG	AGCGAGTACA	AACTCTCAGA	AAACAACTGG	180
ACTAGGGTTG	CAGTTTTGC	AGGCGGAAAC	CGCGGTCAATT	ATCGGACAGA	TTTTGATGCT	240
TTTGTGGGG	TGGATCGAGG	CTCGCTCTGG	GTCTTGGAAAG	AAGACTTACC	TCTTGCTCTA	300
GCAGTCGGAG	ATTTGATTC	TGTGACGGAA	GAAGAGCGAC	AGGTGATTCA	AAAACGTGCC	360
CAGTATTTG	TCCAAGCCCC	GCCAGAAAAA	GATGATACTG	ATTTGGAATT	GGCTCTCTTA	420
ACCATCTTG	AACAAAATCC	TCAGGCTGAG	GTCACTATT	TCGGTGCCTT	GGGTGGCCGT	480
ATTGACCATA	TGTTGGCCAA	TGTTCTTCT	ACCTAGCAAT	CCCTAAGTTG	GCACCCCTATA	540
TGCCTTCNAA	TAGAAATTGA	GGAATGGGCA	AATTGATTG	CCTATTGTTG	CAGAAGGGAA	600
CAGTCAGATT	CGAATCCCTG	CA				622

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

CTATTATCAG	CACTTTATA	CCTATTACCA	AAAAAATCCT	AAAAATGATT	GGCAAAAGGC	60
TTTATCCACC	AGCCATTAT	CAGCAATATT	TACTTGAAAA	ATATGGTAGA	AATAGAAAGG	120
ATGGAGGAAT	CTAATGGTAT	TACAAAGAAA	TGAAATAAT	GAAAAGATA	CATGGGATCT	180
ATCAAACGATC	TACCCAACTG	ACCAGGCTTG	GGAAGAAGCC	TTAAAAGATT	TAACAGAACCA	240
ATTGGAGACA	GTAGCCCAGT	ATGAAGGCCA	TCTCTTGGAT	AGTGCGGATA	ACCTACTAGT	300
AAATCACTGA	ATTTCTCTT	GAAATGGAAC	GCCAGATGGA	GAAGCTTAC	GTTTATGCTC	360
ATATGAAGAA	TGACCAGGAT	ACACGTGTA	GCTAAGTATC	AAGAGTACTA	TGCCAAGGCC	420
ATGACACTCC	TACAGCCAGT	TAGACCAAGC	CTTTCATTC	TATGATCCTG	AATTATGGA	480
TATTAGCGAA	AAGCAGT					497

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

CTGTTATGGA	GTTGAAAGAA	GAATACCACC	CAGACGGTAA	AGGTTTGAA	ATGATCTGTA	60
TCGGTGGGAT	GGGAGCTGAT	TTCTTTAAGG	CTCGCGGTAT	TCAACCACTT	TATGAATTAC	120
GTGGCTTGTC	AGACCAACCT	AGCTTGTATC	AAGTTCGTAA	GATTATTTCA	AAAACTGTTG	180
AAATGTACCA	AAATGAACTC	TTTGATGAGC	TTTATGTTG	CTACAACCAC	CATGTCAATA	240
CGCTAACCAAG	TCNAATGCGT	GTGGAACAAA	TGCTTCCGAT	TGTTGACTTG	GATCCAAATG	300
AAGCGGATGA	AGANTACAGC	TTGACTTTG	AAATTGGGAA	ACCAGCCGAG	AAGAAATTCT	360
GGAGCAGTTG	TTGCCTCAGT	TTGCAGAAAG	TATGATTTAC	GGTGCCATTA	TCGATGCCAA	420
GACAGCTGAG	AATGCTGCGG	GTATGACAGC	CATGCAAACA	GCGACAGATA	ATGCTAAGAA	480
AGTCATCAAT	GATTTGACAA	TTCAGTATAA	CCGTGCCAG	ACAGGCGGAT	ATTACACAAG	540
AAATTACCGA	AATCGTAGCA	GTGCCTAATG	CCTTAGAATA	GCTCTAGTCC	CAGCTCTCCT	600
CACTC						605

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

CTACACTTGA	GGGAAGTTG	AAAATTCCAT	TTTTCTTAAA	GGGAATTGTG	AAACGCTATG	60
TATTTCTTT	TTACAAACCGG	ATGGAGCACT	TGGTTGTGGT	CAATCCTATG	TTTATTGAGG	120
ATTTGGTAGC	AGCTGGTATT	CCACGTAAA	AAAGTGCACCA	TATTCTAAC	TTTGTCAACA	180
AGGGAAAAAT	GGCATCCTCT	ACCACAAGAA	GAGGTAGTCA	GACTGCGCAC	AGATCTGGT	240
CTTAGTGACA	ATCAGTTAT	CGTAGTAGGT	GCTGGGCAAG	TTCAGAAACG	TAAAGGGATT	300
GATGACTTTA	TCCGTCTGGC	TGAGGAATTG	CCTCAGATTA	CCTTTATCTG	GGCTGGTGGC	360
TTCTCTTTG	GTGGTATGAC	AGATGGTTAT	GAACACTATA	AGAAAATTAT	GGAAAATCCC	420
CCTAAAAATT	TGATTTTCC	AGGCATTGTA	TCGCCAGAGC	GGATGCGCGA	AATTGTATGC	480
TCTAACGGAT	CTTTCTTGT	TGCCTAATTA	CAATGAG			517

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

TGTTCGCCTC	CATATCCNAA	ACTTGCCCTG	CCACCATAACC	CAGACTACCT	GAAGCAAGGG	60
ATAAGTTGGC	AATCGAGCCC	ACCTNGATCT	GACTTGGCGA	ATCTGCCTGC	GCAATCAAGG	120
CATATGGGTG	TAAGAATAAG	GATCTCCAGC	CAAATGGCC	ATAGCTTCAC	CGAATTCTTN	180
GTGATTGGTT	AACCGCCCTC	TTCGATAATC	GTCATCATCC	ATAGCAGGAA	GGTCATCGTG	240
AATCAAGCTC	CCTGTATGAA	TCATCTCCAA	GGCAGTAGCT	ACCTGCGCGN	GAGCAGGTTT	300
GATGGTAACC	TGCAAGGCTT	CCAGAACCTC	TAACAAGAGA	AAAGGCCGAA	TACGCTTGCC	360
ACCAGCATGA	ATAGAATAGA	GAACAGACTC	CCGTAAACTA	GAGGCAAAC	GCTGGTCTCC	420
ATAAAATCTT	CCAAAGCCGA	CTCGACAAGA	GCTAATT	TTTCTT	CATTCAAAAT	480
CACTTTCTGT	TCCGTCTTCT	TGCATGACCT	TGACCAAGGT	CTTTTCAGCC	TTGTCCAGCG	540
TAGCTTGGAG	CTCTTTGAC	AAGACCATGC	CCTTTGAAA	GGCAGTAATC	GCATCTTCCA	600
GAGCAATTTC	ACCATTTCC	AAACTTGGA	CAATGGTTTC	CAGTTCTGCT	AGATTTCCT	660
CAAATTCTT	TTGTTTGAC	ATCTTTAACC	TCTAATTCTA	CTTGACCATC	TCGCATCAAA	720
AGCGTTACTT	GGTCTTTTTT	CTTCAAACTC	TCAACCGAAT	CTACAACGGA	TCTTCTTTT	780
TGACAATAGC	ATAACCAC					798

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 547 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

CCATGTTTGC	GGCAGTGACA	GCAGGTTATC	AGGCTGCCCT	AATGGTACCA	ACAGAAATCC	60
TCGCAGAGCA	ACACTTGAG	AGTTTACAGA	ACCTTTTCC	CAATTGAAA	CTGGCTCTCT	120
TGACAGGTTG	CTTGAAAGCT	GCAGAAAAGA	GAGAAGTCTT	GGAGACCATT	GCCAAGGGTG	180
AGGCTGATTT	GATTATAGGA	ACTCACGCTC	TGATACAAGA	TGGGGTGGAG	TATGCTCGTC	240
TTGGTTTGAT	TATTATCGAT	GAGCAGCACC	GTGTTGGTGT	AGGGCAAAGG	CGTATTTAC	300
GGGAAAAAGG	CGACAATCCA	GATGTCCTCA	TGATGACGGC	GAATCCCATT	CCACGGACGC	360
TTGCCATCAC	AGCCTTGGA	GATATGGATG	TTTCCATTAT	CGACCAGATG	CCAGCAGGTC	420
GGAAAGCCCTA	TTGTGACGCG	CTGGATCAA	CATGAGAAC	TACCTCAGGT	CTTGACTTGG	480
TTAGAGGGGG	AAATTAAAAA	AGGTTCCCAA	GTCTATGTCA	TCTCTCCTTT	GATTGAAGAA	540

TCAGAAG

547

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

CTCTTTAAC CGTTTAGCG GTGACACCGA GGTATTTTT CAGGACCCAA GACTTGTGG	60
GCAACCGAAA CTGGGAGTTC GTCATCTCCA ATATGCAGAC CAGCAGCATC AACCGCAAGA	120
CAAACATCCA ACCGATCATC GATTATCAAG GGGACCTGAT AGGCATCTGT TATTCCTTG	180
ACTTGTGGTCCAGTTGATA ATATTGATTG GTTGTGAGAT TTTTTCTCG CAATTGGACT	240
ATGGTAACCC CTGAACGGCA GGCGTCTCA ACTTTGCAA GAAAGCTTTC CACGGAATCT	300
TGATAGCGAT TGTTTACCAAG ATATAGTCTA AGCGCTCTC TATTCATAAA CCTCTCCTT	360
GATGGTATCT AGCCAATTTT CATCTCTCT TAGGAGCGAA AGCTGATTGA GTACTTGGTA	420
ACGAAATTCT TCCAATCCC TTCCTTGAAC AACTATTTC TCAGCCAGCG ATATTGAGAT	480
AAGAGACTGC TAAGCAAGAA CTTCAAAACC AGTCTTCCT TGGCTGAGAA AAACAG	536

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 854 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

CTGGAGTGAC GATTGAGAAA ATCTTGCCC TAGAAAATTA TCGAAATCAG TTAGCTGCTT	60
TTCCGAAAC TGTCTGGATT TCAGAGGATA TTTTGCTAGA TTTGGCGGAT TCTCAGACTC	120
CACAGGGAAAT TGTTGCCGTG GTTCAAAAG AAGAAGTAGG ACAAGCTGAT TTGAGTCAGG	180
GCAAGTTCTT GTTTTGAA GATGTGCAAG ATCCTGGTAA TGTAGGAACATCATTGAA	240
CTGCGGATGC AGCAGGTTT ACAGGAGTGA TTGTTTCAGA TAAGTCGGCA GACATCTACA	300
GTCTTCAAAA CCCTACGTTT CATGCAAGGT AGTCATTCC ATCTGCCAT TTACCGGATG	360
ACTAGTCAAG CGCTTCTTGA CGAAACTAAA AAGGTAGCTA TCCCAGTGCT AGCAACAACC	420
CAATCTAAAG ATTCTGTTGA TTACAGAGAA CTGCCTTCTA TAGAAAATTT TGTACTAGTT	480

ATGGGAAATG	AGGGTCAAGG	AATTAGTCCC	CTTATGGCTG	AAAGTGCAGA	CCAGTTGGTC	540
CATATTAGCA	TGAAGGGGCA	GGCCGAGAGT	TTGAATGTTG	CGGTTGCAGC	CGGTATTTA	600
ATCTTCCATT	TAAGCTAATT	TTAACTTTT	TTGTTATAAT	CAAGGAAAGA	TGTTCACAGA	660
AAAGGAGAAA	TGGATGAATC	ACACTATTAT	ACATGACCCT	GCAGGTCTCA	ATCAATTTA	720
CGCTAAGGTT	TATGCCCTTG	TTGGTCTGGG	AATCGGACTA	TCTGCTTTGG	TATCAGGCCT	780
TATGTTGACG	GTCCTTCAGT	CTCAGTTGGT	TTACTTTTG	ATGCAGGGGC	GTCTCTGGTT	840
GACCATTGCT	ACTT					854

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

CTGAAGAAAT	CCTAAAAGAT	TTGTATTACG	GAGCCGCTAA	AAAAATTCAA	GAAGAAGCCT	60
CTCGCTGGGC	AGGAGTTGTA	AGAAATGACT	AAAACAGCCT	TTTTATTGTC	TGGTCAAGGT	120
GCCCCAGTATC	TACGGATGGG	ACGGGATTTC	TATGATCAGT	ATCCGATTGT	CAAAGAAACG	180
ATTGATCGAG	CGAGTCAGGT	GCTCGGTTAT	GATTTACGTT	ATCTCATCGA	TACGGAAGAA	240
GACAAACTCA	ATCAGACCCG	CTATACGCAA	CCAGCCATT	TAGCGACTTC	GGTTGCTATC	300
TACCGTTTAT	TGCAAGAAAA	GGGCTATCAC	CCTGATATGG	TTGCTGGTTT	GTCTCTTGGGA	360
GAATACTCTG	CCTTGGTGGC	AAGCGGCGCC	TTGGATTTC	AAGATGCCGT	TGCCTTGGTA	420
GCTAAGCGTG	GAGCCTATAT	GGAAGAAGCG	GCTCCTGCTG	ACTCTGGCAA	GATGGTAGCA	480
GTTCTCCATA	CCCCGTAGAG	TCCTTGAGAA	GCCTGTCCAA	AGCTCTGACT	TGAGTGGTAC	540
TCCAGCCACT	ATACACACTG	CACAATCTCA	TTGCTGGAAA	ATTGTTGCAG	TGATCAACGG	600
TGACTTTGCA	GAGCAGTGCC	AACCCTATCC	CCTAGT			636

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

CTCTAAAACG AATTCTCTAC AAGCACCGCA AGGGCATGGC TGAACCTCCA CCATAAGGTG	60
GTTTGTCTCG AAAGGCTAAT ACTTCNTTAA CCTTAGTTG TCCTGAAAAT TGGTACATAT	120
TGAAGAGGGC CGCCCGTTCT GCGCAGAGAT GGAAAACACC ACAGGTTCCC TCCATACAGA	180
ATCCTGTAAA TATTGTCCA TCTCCTGCTT CTACTGCAGC TACAACATGA TTGGCATAAA	240
CAAAGTCTGA TACTTCATGT GGATTGTATA GTTTCTGTGC TTCTTCCTAC ATCTTTCCC	300
AGATGTCCAT TATTGTATCC TCTATATTAA GAGATTCTT TTAGAATGTT TTCGATATGC	360
TGAATTGATT TTTCACGTCC AAGCAAGAAA ATTGTATCTG GTAATTCTGG CCCATGCATT	420
TCGCCTGAAA CTGCGATAAG AATAGGCATG AAAAGATTT TCCCTTAAT ACCTGTTCT	480
TTTTGGACTG CTTTAATTG CGGGAAGATA TTTCTGTCA CAAATTCAATC ATCTGTCAATC	540
CGCTTCAATT TTTGCTTGA ATGCTCAAG AACTGTTGGA ACTGTTTCAC CCGTCATGAC	600
TCGCGCTCT GCTTCTGTCA ATTCTGGGA AATCTGAGAA GAAAGATCTG TCCATGGGAT	660
ATCTCATCTA CTGATTCTATT GTGGTTTATA GAG	693

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

CTGACAAAGG AGACGGGTAT GGAACAAACA TTCTTTATCA TCAAACCAGA TGGTGTAAAA	60
AGAGGGCTAG TGGGTGAAGT GTTAAAGCGC ATCGAACAAAC GTGGATTTAC AATCGAAAAAA	120
TTGGAGTTTC GTTCACAGGT TTTCAGAAGA GTAGATTGAC CAGCACTATC AGGACCTGGT	180
TGGTCAGAGT TTTTACCCAC CGATTCTGA ATTCACTGACT TCAGGTCCAG TTCTTGTGGG	240
TGTCATTCTC GGTCCTCAAAG TAATCGAAAC TTGGCGGACC ATGATGGGTG CAACTCGTCC	300
AGAAGAAGCT TTACCCAGGCA CTATTCGAGG TGATTTGCA AAAGCTGCTG GAGAAAATGA	360
GATTATCAA AATGTTGTAC ATGGTCAGA TTCCGAGAAG AATCAGCTAA GCCGAGAAAT	420
TGCTCCTTTG GTTTAAAGAG TGGATTGGCT CAATCAATTG GATAAAAGCT CATTGAAATA	480
GAAAGTATAG TCAATTAGTT TAAGACATGA CGCATGATAAT CAAACTTTT AGTTTTGAT	540
ATGGTGCGTT TTT	553

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 488 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

CTAGAGATT	NCGAAGAGTA	TTATTGTACT	TTAAAGGTCT	TGAGATAATT	GTCTTNCCT	60
ACTTGACCTT	CGAAGGTTTT	ACCATTTCA	AGGTAGGAA	GGTCATCGGA	TACTGAAGCC	120
TTGACCTTGT	ATATCTTGCC	ATCAAACTTA	AAGAAGTAGA	CAGTGTCTCC	CTTGATAACA	180
GCTGATTTGA	GGTCTGCTAC	TACTCCCTG	ATGCTTCTG	TCGTTGCATT	GTCAATTCA	240
AGGTGTTTT	TATTGGCATA	CTTGCTGAGC	ATCTCTTCCA	CTGTAGTAGC	AACGATAACA	300
TTTTGGTACT	CGACTGCGTC	TACCAGGGCG	TACTCTTGA	CCAAGCCAGC	ATTGTCCCTT	360
AAGCCCATGA	TGTAAAGAGG	CTTGTCAATTG	AGGTTGATAA	AGATTGGGGA	AAGGTTGCTT	420
TGTAGGATT	CTCCTGAACA	GCACCTTCTG	CTGATTCAAG	GGCTGATTCT	TCTGTCGAG	480
AAGCCAAG						488

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

TACAGCTATC	GGGTCCGTCT	GGTAGTTGGT	CCTCAGAAC	TTCACTGCCA	CTTCTTCCCC	60
ATCTAAGATT	AAGTCTTTGG	CTAGGTAGAC	ATCCGCCATG	CCTCCTCGAC	CAATCTGTTT	120
GACAATCCGA	TAGCGTCCGG	CAAAAATCTT	GCCGATTTGG	ATCATTCTTC	ATCCTCCTCG	180
TTCATAGAAA	CAAGGGCAAC	CGTAATGTTG	TCTAAACCTC	CTGCATTGTT	AGCAAAACGA	240
ACAAGTGTCT	CCGTTTTATC	TGCTAAAGGA	ATATCACTGG	TTACAATATC	ACGAATCTCA	300
CTGCCTGAAA	TCATGTTGGT	CAAGCCGTCA	CTATTGAGCA	AGAGATAGTC	ACCTGACTCA	360
AGGATAACTG	TCCCCAAATC	AGGCTGAATT	TCATCTTTT	GCCCAATAGA	CTGGGTGATA	420
ATATTTTTT	GTGGATGACT	TCTGCCTCTT	CTGGTGTCAA	TTGACCAGCC	TTGAGCAATT	480
CATTAACCAA	AGAATGATCG	CTCGTCAACT	GATGGTATCT	TCTCCACGAA	TCAAGCCGAT	540
ACG						543

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

CTTTAAGGAA AATCAAATCT CTCATGCTGA TACCTCTCCT CATTAAATTA AATAGTAAAA	60
AAGATTCTAT CTCACTCCCT GATTATTACA AAACCATTGA AATATCACAA CTAATAGGCT	120
AGAATGGACA TAGTAAGATN TAGTAGATGA GTCAATTCTAC TCAAATCCAC GTTAGAAAAGG	180
ACTGCTATGC CAGACAATCT CGCGCTTCGC ATGCGCCCTA AAACCATCGA CCAGGTCATC	240
GGTCAGGAGC NTCTGGTCGG ACCTGGAAAA ATCATCCGCC GCATGGTGGA AGCCAACCGC	300
CTGTCCCTCCA TGATTCTATA TGGCCCTCCT GGAATCGGCA AAACCAGTAT TGCCTCTGCC	360
ATCGCTGGAA CGACCAAGTA TGCCTTTCGA ACTTTCAATG CGACAGTGTGA TAGTTAAAAAA	420
GCGACTGCNA GAAATCTCGG AAGAAGCTAA ATTTNCTGGT GGTCTCGTCC TATTGCTAGA	480
CGANATTCA CGACTAGATA GACC	504

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

CTAATAGAGG CGAAAAAATT TCAGGTCCCTC CTTTGCTAGA TGATAATGAG GAAACTAAGA	60
TTTTACCAAC CTCTTCTTCC CGTTTTGGTT ATGCCAATCC TAAGGATCAT GGTTTTAGCC	120
AGGAAACCTT GAAGATTCAAG GTCGAACCAT CTATTCATAA AAGCCGTCGT ATTGAAAATA	180
CCAAGAGAAA TGTCTTCAAT TCTAAGTTGA ATAAAATCTT ATTTGCGGTC ATCTTTCTCT	240
TGATTTTGCT TGTTTAGCA ATGAAACTTT TGTAAATAGAA AAGGAATTGA AATGAAAATA	300
GBAATTATTG CTGCTATGCC AGAAGAACTG GCTTATCTGG TCCAGCATT AGATAATGCC	360
CAGGAGCAAG TTGTTTGGG GAATACCTAT CATACAGGAA ACCATTGCTT CTCATGAAAG	420
TCGTTCTTGT TAAAAGTGG AATTGGTAAG GTCATGTCTG CTATGAATTG TGTGGCGAAT	480
TTTGGCTGAT CATTCCAGG TTGGATGCC TTATTAATAC GGGTCAG	528

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

CTAATAAGAC	TGAAAAGAAG	TCCAGCCAGA	TGTCCCTAAA	AATACAGAAA	AAACATTAAA	60
ACCAAAGGAA	ATCAAATTAA	ATTCTTGGGA	AGAATTGTTA	AAATGGGAAC	CAGGTGCTCG	120
TGAAGATGAT	GCTATTAACC	GCGGATCTGT	TGTCCCTCGCT	TCACGTCGGA	CGGTCATTTA	180
GTCAATGAAA	AAGCTAGCAA	GGAAGCAAAA	GTTCAAGCCT	TATCAAACAC	CAATTCTAAA	240
GCAAAAGACC	ATGCTTCTGT	TGGTGGAGAA	GAGTTCAAGG	CCTATGCTTT	TGACTATTGG	300
CAATATCTAG	ATTCAATGGT	CTTCTGGGAA	GGTCTCGTAC	CAACTCCTGA	CGTTATTGAT	360
GCAGGTCACG	TAACGGGGTT	CCTGTATACG	GTACACTCTT	CTTCAACTGG	TCTAATAGTA	420
TTGCAGATCA	AGAAAGATT	GCTGAAGCTT	TGAAGCAAGA	CGCAGATGGT	AG	472

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

CTTTTAAATA	AGAAGAATCA	CACTCATTC	TAAATGTGAT	ATAATATTGT	TCTCAGTCTC	60
AGCAGTGCCT	TGTAAAAAG	CCATACTAAT	CCCTGATTTT	TCCGCATATT	CCATCACCTC	120
AAGTGTGTTA	CTCACTGAGC	CAACTTGATT	AGGCTTTATT	ACAATACCAT	CAGCACAAATC	180
TTTAAACTGT	GAAATTCTTT	CTAAGTTGT	TGCGTAAAAAA	TCATCACCAA	AAACTTGTA	240
CTTTAGAGGT	TTTATCAATT	GAAATTCTCT	CCAACTATCC	AAATCTTCAT	CGGAAAATGG	300
ATCTTCAAGA	TAAACCAATG	GATACTAAC	TCCCCAATCA	CAATAAGTAT	CCATAATTTC	360
TGTGACTGTC	TGTTGCTGAC	TAACACACCA	TGGTACTTTA	TATATGCCAA	GTGAAGAAC	420
GTAACGATCT	GTCATTGCTA	AATCTAAACC	GATATCATAT	CTATTTTGT	ATAATTTAA	480
TGTCTCTAA	AACGAATCCA	AAATAATATA	AAAATCATCC	GTGTTAATTA	TTAATGCACC	540
TTGATAGAAA	TAGATGTTGT	AGAAACCTGG	GTTTTAACTT	TATCATAACT	CATTTTTATG	600
TTAGA						605

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

CTGAAGAAAA	TCAGTAAACA	AGAGCTGGTT	AACACCGCCT	TTTCTCGTTT	ATTTGCTCAT	60
TTTGGACAGG	AAAAAGACGG	TAGTTTTCTT	GCCCAGCGTT	ACCAATTATA	CCTCGCCCG	120
CAGGGACAAA	CACTATCGGG	CGCTCATGAT	CTCTTGACAA	GCCTCATTGA	GCGTGATTAT	180
AACTTGTATG	CTGCGACAAA	TGGCATTACT	GCCATTCAAGA	CAGGACGTTT	GGCTCAATCT	240
GGTCTAGCAC	CTTATTTCAA	TCAAGTCTTT	ATCTCAGAAC	AGTTGCAAAC	TCAAAAGCCG	300
GATGCTCTTT	TTTATGAAAA	GATTGGCCAG	CAAATTGCTG	GATTTAGTAA	AGAAAAGACC	360
TGATGATTGG	AGATTCTCTA	ACCGCCGACA	TTCAAGGTGG	CAATAATGCG	GGGATTGACA	420
CTATCTGGTA	TAATCCTCAT	CACCTCGAAA	ATCACACACA	AGCCCAGCCG	ACTTACGAAG	480
TCTATTCTTA	CCAAGACTTG	CTGGATTGTT	TAGATAAAAA	TATTCTTGAA	AGATCACGTT	540
TTAAGGAGAT	AG					552

(2) INFORMATION FOR SEO ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

CTTTGTCTGT	ATCTGCCCTT	TTATGCTATA	CTTAAGGTAT	GCATAGAAAA	ACAGTGATTG	60
ATTNTAGGAC	TTTAGGGGAG	AGATATACTT	TTACCCANCC	TATTAAAGAG	TTGAAAACGA	120
GAAATGTAGC	AGAAGTGGCA	GATTGCTGG	CACNAGTGGA	AAGCTACCAA	GAGCAAGATT	180
ATTATGTGGT	GGGGTATGTC	AGCTACGAGG	CTGCACCTGC	TTTTGAGGAG	AAATTAGCAG	240
TTCACAAGGT	TCCTCTACTG	GGCGAGTACT	TGCTTTACTT	TACTGTTCACT	GATAGGGTGG	300
AGACCTCCCC	TATTCCTCTG	ACTTATGAGG	ATATTGATT	GCCCTCAAAT	TGGCAGGGAA	360
NTAACGTCTG	CACAGAACTA	TGANAAGGCC	ATTGCCCAAGA	TACAC		405

(2) INFORMATION FOR SEO ID NO:168:

(i) SEQUENCE CHARACTERISTICS.

- (A) LENGTH: 524 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

CTCAAAAACA GCTTCTAACAA	GGGGGCTAAA ATTGATTCCCT	TGATGTAGGG	60
TTTGAAGTAA GATAATAGGT	GTTCATCTAAA TCCCTTCTAT	TCATATTCTA GAAATGAAGA	120
AAGTGGGAAG CCCCACTCTC	TGTTTATTT GTTTAAGTAA	GGCAATAGAT AGCCATATCC	180
TGCTTTTCC ATCTCATCCT	TGGCACAAA GCGTAAAGAA	GCAGAATTGA TACAGTAACG	240
GAGGCCGCCT AACCTCCGCG	GTCCATCTGT GAAAACATGA	CCCAAGTGAG CACTGCCTGA	300
ACGAGAACGA ACTTCAATT	GCTCCATTCC ATGGCTCAGA	TCCTTGTAAAT AATGAATCAA	360
CTCTTTGGAA ATCGGACGGC	TTAAAACTTG GCCAACCCAC	AACCTGAAGC AAACATTATCC	420
TTGGCAAAAA AGAGTTGGCT	CACCTGTTCG TAATATCTAC	ATAAATCCCC TCCTTCCAAA	480
GGTTTTGGTC CATAGGCATT	GGTAAATGGA CCTCCTGTTA	CCAG	524

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 593 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

CTTCATCTGG TGGTTCTCCA	GTGTAAGTA ACGTAGTACC	ATTCTCAAAA CCATACTCAC	60
AAGTTGGTAT	TAAGGGGAA CCATATATCT	TTAAAGGAAT GAAATTGCAA AAAGATATTG	120
TTACAACAAA AGAATATAAC	GAGGTTTAA AAAATGGCAA	AAAGAAAAAT TGGAATCCAA	180
TAGCAAATAC CAAAAAGAAC	TAGAAAAATA CATTAATAA	GGAATGGTAT TGATCTTGAT	240
AAAATTTTA AAATACTGTC	ATTTGAATA TAAAGGAGTT	TGATATGGAG TGGATTAGAT	300
TAATAGGAAT AGCAATCATT	GTTGTGGTT TTATTTAAA	ATTTGATACA ATTGCAACAG	360
TAGTCTTAGC TGGTTGGTT	ACAGCTTAG TTTCAGGTGT	TTCTCTCGTT GAATTTTGG	420
AGATTTGGG AAAAGAATT	AGCAATCAGC GAGTGCTCAC	GATTTTATG GTTACCTTGC	480
CTCTTGTGGG GCTGTCAGAA	ACCTTGGAC TCAACAACGA	TCAATCGATT TGATTCGAAA	540
GATTAAAGGT CTGACAGTTG	GAAACTTCTA TACAGTTAT	TCTTATCGA GAG	593

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

CCTGCTCCTT ATCTTTGCAG TAATTGGCGT TTTAGTGGCC TTGATAGCTC AATTTTACTC	60
AGCAAAGGCA GCAGTAGGTT TTGCTAAGGA ATTGACAAAC GATCTTATC GTCAATTCTCT	120
TTCCTTGCCC AAGGACAGCA GAGACCGTCT GACAACCTCT AGTTGGTTA CTCGCTTGAC	180
TTCGGATACC TACCAAGATTC AGACTGGTAT CAATCAATTCT CTGCGTCTCT TTTTACGAGC	240
GCCCCATTATC GTTTTTGGTG CCATTTTAT GGCTTATCGA ATCTCAGCTG AGTTGACTTT	300
CTGGTTCTTA GTCATGGTTG CCATTTTGAC CATTGTCAATT GTTAGGGTTA TCTCGATTGG	360
TCAATCCTCT CTACAGTAGT CTCAGAAAGA AAACCGAACCC ACTGGGTTCA NGAAACCCCC	420
CNCCATTGCA AGGATGCCGG GTTATTCCGT GCCTTT	456

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 565 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

CTTGTACAGT TGAATCGTTC AGATATTGAT TTTGAAAACA GAGAGTGTGT TGTCTTTGGT	60
AAAGGAAAGA AGGAGAGACC AGTATATTGAT GACGCTCGGA CGAAAATTCA TTTAAGAAAT	120
TATCTTAACG ACAGAAAAAG ATAGTCACCC TGCTCTTTT GTAACGCTAG TTGGAAAAGC	180
CCAGAGACTT GGAATTGCTG GTGTAGAGAT TCGCTTAAGA AAGTTAGGAG ACAAACTCGG	240
CATAACAAAG GTTCACCCAC ATAAGTTCAAG AAGAACTTTA GCGACTAAGG CAATTGATAA	300
AGGTATGCCT ATCGAACAAAG TCCAAAAACT GCTAGGTCAT AGCAAGATTG ACACAACCCCT	360
GGCCTATGCC ATGGTCAATC AAAATAATGT CAAGCATTCA CACCAAAAT TCATCTCTTA	420
AAAGCAAATC CCGATATTCC GAAGAGGTGG TTGCATGAAG AAAGTGAAT TAGGTGAAGT	480
GGCTACTTTT ATCAATGGCT ATGCTTTAA ACCTCAAGAT TGGTCCTCTG AAGGAAAGAG	540
ATTATCCGAA TTACCGAATC TGACT	565

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

CTTTATACTT TATCATTCT AACTTAATTA TAGTCTTATT TTTAATAAAAG TTCAATTATT	60
TATATGTAAA ATTCCCTCATC AGTAAAAAAT AACCGATCTC ATTTCTGAGA ATCGGTTTC	120
TAAATAAAC AAACCGATCA TTTACATAAC ATAAATTATG TAAATGATCA TACTACAACA	180
ACAAATCTT GACTTTCCA ATTTCACTTT TTGGAATAAC CAGGTGAATC ATATCACCCA	240
GATACATTCT GGTTGAGCCG TTAACTGTTT GGCTCTTGCC ATTATGGACT TGAGTTGTGA	300
TGAGGACGTT GTGTGGTAAG TTGAGTTCAT GAACTTGTAA CCCAGCAATT TTATCAGAAA	360
CTGGTATTTG GATAAGTGTAA CTCTCTCCTT CGCTAGATAC TTCTCTGGG AAGCATTGTT	420
TCCAGCATGG CTTCATAGAC TGGCGTTCTT TTGAGCNAAT CCCTGATNAT TTTAGAAACC	480
AGAGTGACAG ACCAGTGGCT TAAGGTGCGA ATATCTCCTA CCATCTCAGT TACGAGAT	538

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

CGTGCTAACCT ATGAGAGCAT ATATTCCTC CAACTATTTC TATTTCAAAA AATCCTTACT	60
ATATTGTATC ACAATCAGAC ACAAAAAGAA AAAGCAAATG ATAAACAAAT GCTTTTAANG	120
TTTTAAAAAA AGCTTCGAAA GGTTCTTCTT TATTTTTAA NGGGAGAGAT AACGTTGATA	180
TCTAAATCGT GGTCAAAGCC GGCAATTTC CTTTAGATGT GTATTGGTGA ATATCATAAT	240
CTAAATCAGT TTTAGGACTG CTCTCCAAA ATCCTGAGTC TGAGCCGTAG GACGGAATCC	300
AAACAGAGGT AAACTTGCCT GTATCAATAC TGTGTTCTTC CATGAAGTAG ACACCAACGT	360
AGATGCCGAT GTTTTTAGCA CCTAGTGATG CTAGTTTGC TCGAAAGTTT TCGACACCTT	420
CGTTCATATA GACATAGTTT TGTCTCCACG TCAGCCCATA GTAACTAGGC TGTTAGGAGA	480
GCACATTGTA GAAAACCTCG GCAGCCTTT	509

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

CTGTTCTGTT	TGCAGCGCTA	CTTGGTTGTA	GCATGGGGGT	GGTTTTAGAT	GGTCAGTAAG	60
TATCTTTTAT	TAGCAGTTAT	TTTCTCTGGC	TTGGTGACTT	GGATTCTCCG	TATGATTTCC	120
TTCATCTTAG	TCAAGTATAA	GGGCTTGCCT	GCAATCGTTG	AGCGTTTTTT	GAAGTTCTTG	180
CCCGTTTCCA	TTATCTTGC	CTTGATTCTT	TCAAGCGTAG	TGACAGGTAA	GGTTGGGAGC	240
CTTCCTCAAA	TTAAATGGCT	AGACTTCTTA	GCCGTCTTTC	CAACAGCTTG	GGTAGCCTTT	300
CGCTACCGCA	ATCTACTCGG	AACAGTTCTC	TTTGGAGTGG	TCTTGATTGC	CATCTGCGT	360
TTGGTCTCTT	AAATTACCCA	CCAAAAAAAC	TTATCACAGA	GATAGATATC	ATATAATGGC	420
GTAAATGCTC	CTTTTCTGTT	AAGATTATAA	GGTATTCTAT	TTTGGAGGAA	ATGACATGAA	480
AAAAATCGTT	AAATACTCAT	CTCTTGCTGC	CCTAGGACTT	GTTGCTGCAG	TGTGCTTGCG	540
GCTTGCTCAG	GGGTGCTCAG	AAAGAAGAGA	AC			572

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

CTAGGTTATT	TAGTAAAAGA	CTAGAAAGATT	TTCTTTCCC	AATCGTCTTC	TGTACGGCGA	60
GGATAGAAAA	ACTCTGACTT	GTCGGGAGCT	TCCATCATTT	CCATCAATGG	TAGCATATCA	120
TAGGCCAGAT	TTAAGTTTGG	AATCTGGTCT	TTTGACCC	AAGAAAATTC	TCCCTCTTCT	180
GAAGATTGAA	GGGTACCAGA	GAACTCAGTC	GCCTTATAAC	AAATGACAAT	ATAGCGCCCA	240
CCTGTATCTA	GTGGCCAATT	TTTAATGCCG	ACAAGTTGAG	GATTTGGAT	AGTCAACCCT	300
GTTTCTTCGT	AGATTTCACG	AATGACAGAC	TCCGCAAAG	CCTCATCATT	TTCTACATGA	360
CCTCCAGGAA	AGGCATAACC	AGACCAGCGA	TTGTTTCAG	GGGCGCGATA	CTGCATCACC	420
ACGCGCTGAG	TTTCGANGTC	TTCCATCAGA	CAGATATTG	TTTAAATTGT	TTAATTGGGA	480
ACGGGACATA	AATTAC					497

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

CTGAAATTTT GGAAGAAGAA ATCGGTGTAG ATACAGTCCA AAAAATAGGA CGCATCTTGA	60
TTTGTTTAA ACAATCTAGC AAGAAAGAAA ATCGCAAGAT TTCTAAGAAA GTCAAAGAAA	120
TCTAAGATCG AAACCTCCAA TAACTGTTT TATAGAGAAA TAAAGGGGAC TAGCCTATGA	180
CAATCGAACT ATTGACTCCC TTTACCAAGG TAGAGTTGGA GCCAGAAATC AAGGAGAAAA	240
AACGCAAACA AGTTGGGATT TTAGGGGGAA ATTTTAACCC TGTTCACAAAT GCCCATCTCA	300
TTGTTGCGGA TCAAGTACGG CAACAGTGG GACTGGATCA AGTTCTGCTC ATGCCCTGAAT	360
ACCAACCTCC TCACGTTGA TAAAAAGGAA ACCATCCCTG AACACCATCG TCTCAAGATG	420
CTTGA	425

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 418 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

CTGCTATCAA GACAGTATTAA CCGCTGAAAG AAACAGCTTC ACTAGAAGGC GCAATTGAAA	60
AATAAGACGG GATCACGAAC TCCCGTTTT CTATAAAAGA AAGGAAATGG GATGAAAAAA	120
TTAGTCTTTG TCTGTCTGGG AAATATTGTC CGTAGCCCTA TGGCCGAGTT TGTTATGAAA	180
TCAATGACAG ATAACATACGA AATCCAAAGT CGAGCAACTT CCTCTTGGGA ACATGGCAAT	240
CCGATTCTATA AGGGGACTCA GGGAAATTAA CAAGAGTATG AGATTCCTTA TGACAAGAAC	300
AAGACATCGC TTCAGATTAG TAAGGAAGAT TTTGAAGCCT TTGATTATAT TATCGGAATG	360
GACCGCTTCAA ATGTTCCGAC TTACGTCAGA TGTGTCCAGT AGACTGTCAA GATAAGAT	418

(2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 387 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

ACTGTTGAA	AAATATGATT	CGTGGTCGAG	AAATGAATTG	CATTTAAGCA	ATGTAGTTCA	60
GTATATAGAT	TTGGAAATTA	ATGATTAAAC	AAAATAAAGG	AGAAAAAAACA	TGGTTAAATA	120
CGGTGTTGTT	GGAGCAGGGT	ATTTTGGAGC	TGAATTGGCT	CGCTATATGC	AAAAGAAATGA	180
TGGAGCAGAN	ATTACTCTTC	TCTATGATCC	AGATAATGCA	GAGGCATTG	CAGAAGAATT	240
GGGAGCAAAA	GTTAGCAAGT	TCCTTAGATG	AGTTGGTTTC	TAGCGATGAA	GTTAGATTGT	300
GTTATCGTCG	CAACTCCCAA	ATAATCTCA	TAAGGAACCG	GTTATTAAGG	CTGCACAGCA	360
TGGTAAAAAT	GTTTCTGT	TGAAAAAA				387

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 561 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

CTTATGAAAT	CAATCATCAA	AATAATATTG	ATCAGGACTA	TTTAGGTAAA	TTATCTACAA	60
CGATTAATT	GGTAGCAGAA	AAGGAAAATG	CCGTTGAGAT	CCTAGAACAC	TTGAATGTTG	120
TCCCTGTT	GACAGCCCCT	CCAACACAAG	TGCAACGCAA	AAGTATGTTG	GATTTAACAA	180
ATCATATTCA	TAGTCTTTG	CGTAAATACC	GTGATGTTAA	GTTGGGTTA	ATCAATAAAG	240
ATAAAATGGCA	CAATGATTG	CGTCGTTACA	TCGAAATTAT	CATGCAGACA	GACATGATTC	300
GTGAGAAAAA	ATTAAAAAGTG	ACTAACGAAA	TCACGAATGC	TATGGAAATA	TTACAACAGC	360
TCCTTTTGAA	AAGCTGTCCC	TCATTGACG	ACGGAGTATA	AGCGCTTAGC	GCAAGCGCAT	420
GGTCTGAATT	AAAAACAGGC	TAAACCAATC	ACCATGGTA	TGTGGATAGG	TGGTGACCGT	480
GAAGGAAATC	CATTGTTAC	AGCAAAGAAC	TTGAAGCAGT	CTGCACTCAC	TCAGTGTGAA	540
GTCNTCCCTGA	ACTTACTATG	A				561

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

CGACCTAATC ATATTGATA	TGCATTTGCA TCAGCAGATT	TGTTTGAGTA TAAATTACAA	60
TTAGCAGGAC AGACTTGGGG	ATATTTAGAA TTTGAAACAA	ATACAGAAAA ATATGGAAA	120
GTATTGTTAA TTATAAAGGG	TAAGAACGGA CTTACGAACC	AATTCCTTT GGTACAAAAA	180
AATAAGAGTG GCTACTTATT	TGAATATGCT CAGATGAATA	CACTTTATCT TAATCAACAT	240
TCTTCCTACA AAAATGATGA	AGATAGTCAT TCCTTCCAA	TTCAGATGGA GTTAGTTCT	300
GATGAAATGA TTCCAAGAAA	TTGAACAAGC TACTAAAAAT	TCCGAATATC CGAAAAATT	360
ATGATTTAA CTTATGANGC	GGACTCCCAG AAAACAATAT	TATATCTGTT AGATGTTGT	420
TATGCCCTGA TGCCCGAACT	GGTCCAGTTA CACTTGATT	CAGATTGTCC TGAGTATATC	480
CATCCAGTTC CGTACC			496

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

CCACCCCTCTA GCAAGTGGTG	CTAATTCTTA TAGCCTAGAA	AAAAACGAAA TCATCTACCA	60
AAAGTTAAAA AACTTGCTTA	AAAACTGATA AAATACTTGC	CAAACTTTC AGAATCTGAT	120
AGACTAGTAT GGTAACAATC	TATGGCTCGC AAAGAGACCA	TGGCAGAAAG GAAATATTGC	180
AAAATGAAAA AAGATATCCA	TCCAGAAATAT CGCCCAGTTG	TCTTCATGGA CACAACACT	240
GGTTACCAAT TCCTTAGCGG	TTCAACAAAAA CGCTCTAACG	AAACAGTTGA GTTCGAAGGC	300
GAAACTTACC CATTGATCCG	TGTGGAAATT TCATCAGACT	CACACCCATT CTACACTGGA	360
CGTCAAAAGT TCACTCAAGC	AGATGGACGC GTGGATCGTT	TCAACAAAAA ATACGGTCTC	420
AAATAATGAT AAGAGAACAG	TTTCGGCTGT TCTTTTTGT	TTCTTGAAAT CAACTGCTGT	480
TTTCATGTTC CAGACTCATC	TGTA		504

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

CTCAGGCGAT TACTAATTAC ATGACTTCTG CCTCAAACCTT TAATGTCGAT GAGGCTAGCC	60
AATTCAATTCA ACAATTTACA ATTACAAAAC AAATCGAAC AAGTAGAAAAAA CTATTAGAGG	120
AGTAGCATGG AAACCTGCATT AATTAGTGTG ATTGTGCCAG TCTATAATGT GGCGCAGTAC	180
CTAGAAAAAT CGATAGCTTC CATTAGAACAG CAGACCTATC AAAATCTGGA AATTATTCTT	240
GTTGATGATG GTGCAACAGA TGAAAGTGGT CGCTTGTGTG ATTCAATCGC TGAACAAGAT	300
GACAGGGTGT CAGTGCTTCA TAAAAAGAAC GAAGGATTGT CGCAAGCACG AAATGATGGG	360
ATGAAGCCAG GCTCACGGGG ATTATCTGAT TTTTATTGAC TCAGATGATT ATATCCATCC	420
AGAAATGATT CAGAGCTTAT ATGAGCAATT AGTTCAAGAA GATGCCGATG	470

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

CTTATACTTG CTTTTTCCT TTTGAAAAAT GTTAATAAAAT CGTTGGTAGT CTTCTCTAGG	60
CATGGACAGA TCAATATCGT CGTCCCAGG GATAAAGCCC TCATGTCGAA CCCCCCCAAT	120
CAGAGTACCG TAGTTAATAA TATAGTTGAT ATTGTGCTTT TTACAGAGAG TATCAATATA	180
ATCCAAAATT TCTAATTCAA TTTGTTGGC ATCTTCAATG GTTAGTTGTT TCATTTAAA	240
CTCCTATGAT TTTTGAAATT TATTTTTAA GGCTAGGACA TGGTTTAAAA ATTCA TAGAA	300
AATGCTATCT TTTGTGAAGA CAAGTAGACT AATATAAGAG ATAGCTGATA ACAAGACAAT	360
CAAACCAGTA TTAATCAAAA ATGGCAAATT AATGACCATA TCCACAGGAT ACACGAAATT	420
AATCAGGAAA TACATTGCTA CAAAGGAAAG TGAAAAGAGA GAGTATCGAA CAGTATAGCT	480
AAAGATATGT CCCAAGTGGT TGAGTTGTTT CTATGGATGA AATGAT	526

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

ACCATATCAA TACTATCGAA AAGTACAAGG GATNCAGTCT CAAGGGTCGCT GAGGAAGATT	60
TGAATGACCT AGACGATGGT GAATTTTACT ATCACCGAGAT TATCGGTTG GAAGTCTATG	120
AGGGTGATAG CTTGGTTGGA ACCATCAAGG AAAATCCTGC AACCCAGGTGC TAATGATGTC	180
TGGGTGGTCA AACGAAAAGG CAAACGTGAT TTGCTTTAC CTTATATCCC ACCAGTGGTT	240
CTCAATGTTG ATATTCCAAA TAAACGGGTCA GATGTGGAAA TCTTAGAAGG GTTAGACGAT	300
GAAGATTGAT ATTTTAACCC TCTTCCAGA GATGTTTCT CCAGTGGAGC ACTCAATCGT	360
TGGAAAAGGCT CGAGAAAAAG GGCTCTTGG ATATCCCAGT TNTCATAATT TTTCGAANAA	420
AATGCTGAAA AGG	433

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

CTGCAACTTG AATTTCTCCT TCTTGTTCGA AAGCAAGATA AACAAATTGCA GCCCCTCTT	60
TTTCTAGCAA ATCCCCCATC TGGACAGATT GCATAAAGGA ACGAGAAAGAA ACCTGATCAG	120
AATAAGTCTG AAACTCTCTC TTCCGTGAGTG TTGTTAGTGC CATATACTTA CTTTCTATGT	180
TTTTTCTTA ATGTTTTACG GAAATCAAGA GCAAGTCTTA ACAGAGGATA GAGAGGATGA	240
GTGGGCATTG TAAATTCAACC CAAGTATTCT TCAATCGTTG GATTAAATT TTCCCTTAAAA	300
TGATAAAAGTC CACCATTGAG AGAGTTTCA ACACCACTA AATTTTGCCA GACCATAACCT	360
CGCTCAAAGG CATAGCGAGC CGTTTCATAC CATGTTAAA TTGGTGCATT GTAACGTTA	420
AAATCATCAT CCATACCAGC ATATATATTG ACAGAGGTAG TACCAAATTC CAAACTCAA	480
GTACCGCTAA AGGAATCTCG CTTGACCTAC ATCTATATAT TCCTGCAAGA AGGTCAATT	540

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

CTCAGGCTAA AAGAGTCCAC TGGACTCTTT TACTCCGTCC CATAACCAAT GACTTAATGG	60
CGCGTTTCAGC TAGATTATTG GAAAGGACCA GATGTCCGTC TTTCAAAATA GTCTTAAAGG	120
TTTCTTCATA CTTGAGGCTG TATTCAATTG CCCTTCCTAG TTTTGAACCC GATAAAACTG	180
ACTGACGCCG GCACCAAGCA AAGAAATCTT CCATTAGGGG TTGGAGCTCT TCTTGACGTT	240
TCTGTAGTCG TTCATCAGCT GACAATGTCT CCCAGTCTCT TTCCAAGGCA AATAACTGAT	300
CACAATAGGC TAATCCTTTA G	321

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

CTTGACCAAA CAAGGCAGTT GGAAATTGAT TTTGGAGGAT GAGAGCGCTG GAAGGGAACT	60
CTTCCCAATC TTGACTCAAG GTCNATATAT CGCAACATTT GACCAACAAG CGCCANCTAT	120
CGATGAAATC TTTAAACTAT AATCAGGAGT GGAAGTATGA GAAATATGTG GGTTGTAATC	180
AAGGAAACCT ATCTTCNACA TGTCGAGTCA TGGAGTTCT TCTTTATGGT GATTTGCCG	240
TTCCCTCTTT TAGGAATCTC TGTAGGAATT GGGCATCTCC AAGGTTCTTC TATGACTAAA	300
AATAATAAAAG TGGCANTACT GACAACAGTG CCATCTGTAN CATAAGGACT GAAGAATGTA	360
AATGGTGTAA ACTTCGACTA TAAAGATGAA GCAAGTGCCA CCAGAAGCAA TTAAA	415

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

CTATNAAATA GAGTGGTTCT CTATCTGCCA TGACCACAAA TNAGGACAAT GATACTCTG	60
AACGTTTCAGA CTGCTATCGT AAAAGGACAG CGGGTGAGAC GCCCATGAAT GATCTAACCA	120
GTCATACCCA CGGAGGAAAT TATACAATAG CACGTTATCA GGAGGAAAAA TTTTGGAAACA	180
AACAGTTGTA AAATATAGTC TGCAGTTATC AATGCTTAAT TTTTACAGG CGAAGATAAT	240

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

CTTGTCA	TCC	TCACGAAAAT	TGCGATTGTA	AAGCACCAAG	CCTTGACTCG	TGATAGACTG	60
AATCATG	C	CTCTCATGTA	CTCCTCAAGT	CGTTTCATGG	CTTCTTGAT	AGTCTCCATG	120
CTGGCTGC	CAT	AAGATAGGCG	GACGTAGCCT	TCCCCGTAAC	GTCCAAAGGC	TGCACCAGGG	180
ATAAAGG	CAA	CGGCCTTCTT	CTGAGCAAAA	TCCTTCAGAA	AAGCAAAGGA	GTCTTGATTG	240
TAGCCC	GCTG	GAATTTTAGC	AAAAATATAG	AAGGCACCGT	CTGGTTTGAT	AATCTCAAAA	300
CCAAGAG	CAG	TCATTTTTC	GATGATATAG	TCCCAGCTT	GGATATATTC	CTTCTTCATG	360
GGCTCC	G	CGTTTTTACC	AGCCGTCAAG	GCTTCTACCG	CAGCATGTTG	CGCCATGGTA	420
TTTGC	GGCAG	TGACCAAGTT	ACTGGTGACT	CTTGATTAAC	TGGGCTGTGA	AGGTCNCANG	480
AGCAAA	ATC	AGCCCCAAAC	GCCAACCTGT	CATGGCAGT			519

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

CTTCAGCTAT	TCGTGGGATA	TTAGATGTAC	TTATTTAGGG	GTTGAAATCA	TATGAATATT	60
ACCAATTG	T	TTTCTATCAA	GACAGGATGT	GATGAAACTG	ATAGGCAACT	120
TTTTTCAG	T	TGGATTACA	ATTGGGAGAA	TTGACAGATC	AACTAAGAAA	180
AATTTG	TTC	CTCGTAGTCA	ATTGTAGAC	ACGTTGGATT	TGAATGATGT	240
GAAATTTA	A	ACTATTTAT	CTTCCATCGT	AATGATAGTG	AAGAAAGTT	300
TTATATG	A	GGATTTCCAC	AAATCGTTAT	GAACCTCCCT	AAAGAGTTT	360
ATGGCTCC	CAT	AAATACCCAT	GAAAGTGT	CTGAAGTTT	CCGGAGAATG	420
AAACAGTC	CAT	TAGTGACTGT	TTTTTATAGA	AAAGAGTTT	TATATGTT	468

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

CTTGAATAGT CTCATCACGA AAATTGCCAT AACTGATAAA ACCAACCCACC TTACGCCAT	60
CCATCGCAAT CAATGTATTT TCTGGATACT TTTGACTAAA GAATCGACAT CTTTCTAATG	120
TCATTGTATC CTGAAATTCC GCAGGCAAAA GGTCACTCATC AGACTCTCTC CACGTTGCC	180
AGTGAACGAG GGATTTGCCT TCTATCTCTT CAGGAGTTNC CATAGATTG ATAATAACCG	240
TCATTTATTT TCTCCCAGTC TNCTCTCAAA ATACCATATT TAATACTATC AAAATATTTA	300
CCTTGATAAT AACGAACTTT NGGAATATGA GCTNCTTTT TCATNCTTAA TTTTCAGCA	360
AGTTTCATCA TACCAAGATT TCCTGACCAA GTTGTCAAAA CCAGATGCTC CAACTCCAAG	420
TAATCCTGAA ACGTCCTATC TATCCACTGC AACATAGCAA CTTTCCCAAT ACCAGTGTTC	480
CAGAATTTTT TATCATAAAAT ACCAATTCCC AATCCATCCA TCTTGTTC TTTACATACC	540
CAATA	545

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

CTTGATTGTG GAAGAAGTCC GTGATCGCTA TGTGGGCAAA GTCGATGCCG TTTTCATAA	60
CGGCGATTCT GAACTACGTC CGGATTCTCC ACTTTGGAG GGCATCCGCG TTGTTAAAGG	120
GAACATGGAC TTCTACGCCG GCTACCCAGA ACGTCTGGTG ACTGAGCTTG GTTCGACCAA	180
GATTATCCAA ACTCATGGTC ACTTGTGTTGA CATCAATTTC AACTTCAAA AGTTGGACTA	240
CTGGGCTCAG GAGGAAGAGG CCGCTATCTG CCTCTATGGT CACTTGCATG TGCCAAGTGC	300
TTGGTTGGAA GGCAAGATCC TCTTCTAAA TCCAGGCTCT ATCAGTCAAC CACGAGGTAC	360
CATCAGAGAA TGTCTCTATG CTCGTGTGGA GATTGATGAT AGTTACTTCA AAGTGGACTT	420
TTTGACACGA GATCACGAAG TGTATCCAGG TTGTCCAAGG AGTTTAGCCG ATGATGCCAA	480

GGAGTTGAGA CTTTCTGTTG GGGCAGAGAA CTTTTGA

517

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

CGTAACCATT	AACTATGAGG	TGGTTTGCCT	CCTCAGCGAC	CGTATTCCGA	GAGAATATTA	60
TTAGAAAAGA	AAGGAGTGGA	GCATGAATCT	ACATCAACCC	TTGCATGTCT	TGCCTGGTGT	120
GGGACCAAAG	TCAGCAGAAA	AATACGCCAA	ACTAGGAATT	AAAAACTTGC	AAGATCTCTT	180
GCTCTACTTT	CCTTTCCGTT	ATGAAGACTT	CAAAACCAAG	CAGGTGCTGG	AACTAGAAGA	240
CGGTGAGAAG	GCAGTTCTTT	CTGGTCAGGT	AGTGAECTCCT	GCTAGTGTCC	AGTATTATGG	300
TTTCCAAGCC	GCCAATCCGC	CTGCCTTTTT	AGTCCTCCAA	GCCAGGGAAAG	AAGGTTCGTT	360
TTTTTTGGC	GGGTGAAATT	TCCTTTTAA	CCCAGCCCCC	TATCCTGGG	CTTGAATAAA	420
AAATTAGAAA	TTTGGGGAA	CCAACCCCTT	TGGCTTGT			458

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

CCTTACTAGT	TTACTCAATC	TTTACATCGT	TCTTTCGGCA	GTTCAAACTC	AGAATCCACA	60
GCACAGGTAA	TGCAATTACT	GTCTGAAAAT	ATGTTAAAAAA	CCATTCAAGTC	ACTTTCGGTC	120
TGGCAGATTT	ATTTGCTTGG	TTTGAGCGA	ATCTTGGCGC	TTGGTTTCCA	ATTACTTTG	180
ACAGTTGGG	TTTACCAAGC	TGTTGCCAG	AAGAAATGGA	TTTATCTCCT	AGCAGCCTAT	240
GGCTTGCATG	CCTTCTTGA	TCTGGCACCA	TCTCTTTCC	AAGTAGGCTG	GTTGACAAAT	300
CCAGTCTTGG	TTGAAGTGAT	TCTAGCACTG	GAGCTCGTTC	GGTCGCCCTA	TGGAACCAAG	360
GAAATCTTT	GTAAAAAAC	ATAAAAAGGG	GGGAACCTCT	TTTTCTTATG	CAAATCCAA	420
ACAAGGTATT	TTTATGGTCG	TCAAATGTCT	CTAAAATGG	TATAATGGAA	TGAATTTGT	480
AAAAGGAAGA	ATGACATGTC	TGTAAGAGAA	AAAATGCTTG	AAATCTTAGA	AGGAATTGAT	540

ATCCGTTTTA AGGAACCCTT GCATAG

566

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

CTTGACAAA GAGTATGACA CCTGACCGTG AAGTCATTAC CTTTATTCCCT GAAAAATTAA	60
TTGTGGATGG TTTCCAAGGG ATTCTGTGACC CACGTGGCAT GATGGGGGTT CGCCTTGAAA	120
TGCGTGGTTT GCTTTATACA GGACCTCGTA CTATCTTGCA CAATTTGCCT AAGACGGTTG	180
AGCGTGCAGG TGTCAGGTT GAAAATGTTA TCATTTCACCC ACTAGCAATG GTTCAGTCTG	240
TTTGAAACGA AGGGGAACGT GAATTTGGTG CTACAGTGAT TGATATGGGG GCAGGTCAAA	300
CGACTGTGCGC TACAATCCGT AATCAAGAAC TCCAGTTCAC ACATATTCTC CAAGAAGTGG	360
AGATTATGTA ACTAAAGATA TCTCCAAGGT TTTGAAAACC TCTCGCAAAT TAGCGGAAGG	420
CTTGAAACTG AATTACGGGG AACCTATCCG CCTCTTGCAA GCAAAAAACT CCATTAAAGT	480
TATTGGAGAA TTAAACCAGT CAAAGTGACG GAACCTACTT GTC	523

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

CTGTGATTTTC AGAGAAGAAA TCAAGTGCTG TAACAGAAAGT AAGATGTAAT TGTATGTAAGA	60
GGAGACGTCA TGTTAAATAG TATTGTAACC ATTATTTGTA TTGCCCTTAT CGCGTTTATC	120
TTGTTTGGT TTTTCAAAAAA GCCTGAAAAA TCTGGACAAA AAGCCCAGCA AAAAAACGGA	180
TACCAAGAGA TTCTGAGTGGG AGTCATGGGA GGCTATACTC CTGAGTTGAT TGTCTCAAG	240
AAATCAGTGC CAGCCCGCAT TGTCTTGAC CGCAAGGATC CTTCACCATG TCTGGATCAA	300
ATTGTTTTC CAGATTGAGTGG TGTACATGCG AACCTGCCAA TGGGGGAAGA GTATGTAGTG	360
GAAATCACGC CTGAACAGGC TGGAGAGTTT GGCTTTGCTT GTGGTATGAA CATGATGCAC	420
GGCAAGATGA TTGTAGAGTA GGTGGAGACT ATGACAGAAA TTGTGAAAGC AAGCTTAGAA	480

AATGGCATTC AAAAAATCCG TATCCGAGCT GAAAAAGGCT ATCATCCACC CATATCCA

538

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

CCTCAAGAAG	TCCGCGATAAC	TTACGAAAAT	ATTTTGTAGA	GAATCGAAC	GCAAGGTTCG	60	
GT	TTTCTTT	TCTTTTGTC	TATAATTG	GG	AGTATGAAA	TCGTATCAGG	120
AATCTATGGG	GGACGTCCCC	TCAAGACACT	AGAAGGCAAG	ACAACAAGAC	CTACTTCGGA	180	
TAAGGTTAGG	GGAGCCATT	TTAACATGAT	TGGTCCCTAC	TTTGAAGTGG	GACNAGTCTT	240	
GGACCTTTAT	GCAGGTAGTG	GTGGTTTATC	TATCGAAGCA	GTATCGCGTG	GCATGTCCAG	300	
TGCTGTTTG	GTGGAGCGAG	ACCGTAAGGC	TCAGACCATC	GTGGCTGAAA	ATATCCAGAT	360	
GACCAAGGAA	GTTGGAAAAT	TTCAACTCCT	CCAAAATGGA	TGCAGAAAGG	GCATTGGAAC	420	
AGGTTNTCTG	GGGAATTG	CCTCGTTTC	TTAGACCCTC	CCTATGCCAA	GGAACAAATC	480	
GTAGCAGATA	TTGAAAAAT	GGCTGAGAGA	GAGCT			515	

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

CTGGANACAA	ACTTTACAGA	TCAAGTCGAT	ACGATGATT	ATGTTGATAA	AGAAGAAAAA	60
GAAACTATTA	AAGCTGCACT	TGTGGAGTT	TTTAATGGAA	AAAGTCACTT	AACTGACCAA	120
GGTTTACGAG	AGGTTGAAGT	TCCGTAAAC	TTAGTGTAAA	CAATGAATAA	TACAGCGTT	180
CGTTGACATT	CTCACAACTA	CTTAGCGAG	CAAAATAAAA	AGATGCGTAC	CAAAATATAC	240
TAGAAAATGA	AGCAATTCAA	ACGAAACCTG	ATATCGTTT	CCTTCACACC	TATTTACTAG	300
AATTAAC	ACGCAATCAC	TTGAAAATTA	ATGACTTTGG	AT		342

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

CTATTAGCGA	CTTTCTCTGA	AATATGGTAT	GATAAAGGAT	ATACAAGGAG	ATAAAATGAA	60
TAATAATTAA	CTGGTATTAC	AATCCAGACT	TTGGTCTGGT	TGATGGTGC	GTATCGGCTA	120
TGATTGGAGT	GGCTTAGAA	GAGTCTCAA	CCTAAAAAT	CCATCACTTG	ACGCACGATA	180
TCACGCCMTA	TAATATTTT	GAGGGGAGCT	ATCGTCTCTT	TCAGACGGTG	GATTACTGGC	240
CTGAGGGAAC	GACGTTGT	TCGGTTGTG	ATCCAGGTGT	CGGTTCGAAA	CGTAAGAGTG	300
TAGTTGCCAA	GA	CTGCTCAA	AAATCAATAC	ATTGTACACGC	CAGATAATGG	360
TTTATCAAGA	AA	ACACGTTGG	CNTTGTANCC	ATTCTGAGA	TTTCTGAGGT	418
					GGCCA	ACT

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

CTCTCGCTTT	TCTCATAGTG	GGAGGTAAGG	ATGGAATTAC	GCAGACCAAG	ATTAGCGGAT	60
AAGAAAGCTG	TTTTAGATAT	GATGACAGAG	TTTGAAAAGA	GCCAATCAGC	CCATGATGGA	120
GGATTTGGG	ATACAGAGAA	TTTGTGTAT	GAAGAGTGGT	TGGAAAGCAA	TCAGGAACAG	180
GAAATGGGA	TTAATCTGCC	TGAAGGATGG	GTTCCCTGCAA	TTCAGTTAGT	GGCTTTTCT	240
GAGAAAGGTC	AAGCAGTTGG	ATTTCCTTAAT	CTCCGGTTGC	GCCTCAGTAA	CTTTCTACTA	300
GAAGAAGGTG	GGCACATTGG	CTACTCCATC	CGTCCATCTG	AAAGAGGCAA	GGGTTATGCA	360
AAAGAACTCT	CCGTCAGGGC	TTGCAAGTTG	CTAAGGAAAA	GAACATCAAG	AAAGCTCTGG	420
TGACCTGTAG	CGTGAATAAT	CCTGCTAGCA	GAGCATCATT	CTA		463

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

CTCTTACGTG	ACCAGAACAT	GCTACTTCCC	ATCCGAGAAG	CCATTCTATC	TGGCTTACCA	60
GTGTTTGGGA	CCTGTGCGGG	CTTAATTTG	CTGGCTAAGG	AAATCACTTC	TCACAAAGAG	120
AGTTATCTAG	GAACTATGGA	TATGGTGGTC	GAGCGTAATG	CTTATGGGCG	CCAATTANGA	180
AGTTCTNCAC	GGAAGCNNA	TGTAAGGGAG	TTGGCNAGAT	TCCNATGACC	TTTATCCGTG	240
GTCCGATTAT	CAGTACTGTT	GGTGAGGGTG	TANAAATTCT	AGCAACAGTG	AACNATCAAT	300
TTGTTGCNNC	CCAAGANNA	AATATGTTGG	TAAGTCCTTT	TCATCCAGAA	TTGACTGATN	360
ATNTGCGCTT	GCNCCAGTAC	TTTATCAGTA	TGTGTAAAGA	AAAAAGTNGA	GATTGAATT	420
CTCCAACCTT	NCCACNTGTA	ATNNNCAATN	NCNATGTATT	GGAGTACGGA	CGCAG	475

(2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

CCTTCAAAAA	TTATTTGATG	CAACCTTAGA	CAATCCAGAA	CTCACCGCAA	CATTAGTGCC	60
TTTAGGAGAT	GGTATTCTCA	TGCTTCGTAA	AAATGTAGCA	GATGTTCAAC	TGTCTGAAAG	120
CGAATGATTT	TCAGAAAAAT	TTAAGAAAAA	ATAGTAAAAT	AGATAGAGTA	ACACTTATCT	180
CAAAGGAGTA	GACATGAAGA	AAAATTATT	GGCAGGTGCC	ATCACACTAT	TATCAGTAGC	240
AACTTAGCA	GCTTGTTCGA	AAGGGTCAGA	AGGAGCAGAC	CTTATCAGCA	TGAAAGGGGA	300
TGTCATCACA	GAACATCAAT	TTTATGAGCA	AGTAAAAAC	AACCCTTCAG	CCCAGCNAGT	360
CTTGTAAAT	ATGACCATCC	AAAAAGTTT	TGAAAAAAACA	ATATGGCTCA	GAGCTTGATG	420
ATAAAGAGGT	TGATGATACT	ATTGCCGAAG	A			451

(2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

CTATGGATAA	GGCACTTGCT	GACCTCAAAA	CATCAGGGCA	CTTGCCTATT	CCGCGACACC	60
TACGTGATGG	GCAC TACANT	GGAAGCAAGG	AACTGGGGAA	TGCCCAAGAC	TATCTCTATC	120
CACACAACTA	TCCTGNAAT	TGGGTCAAGC	AAGACTATCT	GCCACAAAAA	ATT CGTAATC	180
ATCACTATTT	CCAAGCAGAA	TATACTGGTA	AATATGAACG	GGCTTTGGCT	CAAAGAAAGG	240
AAGCTATCGA	CCATTGCGA	AAAATCTGAA	ATCCTTTCA	AAAAATGCA	CTTTCCTCTT	300
GATTTTTTTT	GAAAAGTGG	TATCATATAA	ATATAGAAC	GCTGTGGTGT	ACGACTTCAC	360
ACTTAAGTGT	TGACCGACTA	TTTTTTGTAT	TATTANGGAA	ACAAAAGTCT	TCTGTCAGCA	420
TGTAGGCCGT	CTCACACGGA	AACAGCTTCA	GTT			453

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

CCGTAGTACA	GGCACAAAAA	GATTTGGAAA	ATAGAAAAAG	AAAAGCCAAG	AAAAGGCTC	60
AGAAAACGAA	ATAAATAAGG	AGGAATCTGG	TAATGGTAGT	ATTTACAGGT	TCAACTGTTG	120
AAGAAGCAAT	CCAGAAAGGA	TTGAAAGAAT	TAGATATTCC	AAGAATGAAG	GCTCATATCA	180
AAGTCATTTC	TAGGGAGAAA	AAAGGCTTTC	TTGGTCTATT	TGGTAAAAAA	CCAGCCCAAG	240
TGGATATTGA	AGCGATTAGT	GAAACGACTG	TTGTCAAAGC	AAATCAACAG	GTAGTAAAG	300
GCGTTCCGAA	AAAAATCAAT	GATTTGAACG	AGCCTGTGAA	GACGGTTAGT	GTAAGAAACC	360
GTTGACCTTG	GTCATGTGGT	TGATGCTATT	AAAAAAATAG	AGGAAGAAGG	TCAAGGTATT	420
TCTGATGAAG	TC					432

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

AAAATCAAGA AATTCTTG A AGGAACGACA GATAAGCTG AGAACTATAT CAAGTCGGCC	60
CTTAAATGT TGGTCAAATA GGAGCAGAGA ATGACAAAAC GTTGTTCGTG GGTCAAGATG	120
ACCAACCCGC TCTACATCGC CTATCATGAT GAGGAGTGGG GTCAGCCCCCT CCATGATGAC	180
CAAGCATTGT TTGAGTTGTT GTGTATGGAA ACCTATCAGG CAGGCCTGTC TTGGGAAACG	240
GTACTCAACA AACGCCAACG TTCCGAGAA GCCTTCCAT AGCTATCAAA TTCACTCCAG	300
TCGCAGAGAT GACTGACACT GAATTGGAAG CCATGCCTGG AGAATCCCAG CTATCATTCC	360
GAAATAGAGC CCAAGATTG TGCTACACGC CGCCTAACGC CCCAACCTT TCCTACAGTT	420
ACAGGCAG	428

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

CTATTAGATG GTATTGACTG CCCAGACACT TACGGATCTA GCTGAGACAG GGAATTGTCC	60
ATAACCTTCC TCATCAATTG TAACTTGACC TTGGTGGTTA CCAAGTAAAT CTACAAAGGT	120
TTGATTAGTC CATTCTTGAC CGACAAACAT TGACTTGCTG TTTTCTTGGT CATTGAAAT	180
CAAGACTGCG ATTGGGGATT GATTTTCAGC ACCTGAACGT ACCCAACCGA TACAGTTAGC	240
ATGGTCAAAG TAGTCATTTT GTTCTCCATA GGCCAAATCT TTTCGGATGG CTAGGAGGCG	300
GTCAAGGATT TCTTTGAAAT CTTGTTGAGC ATACTGGCCT GAAATCCCCT AGTAGTCTCC	360
GTAAAAGACA CATGGAAGGC CGTCTTGGCG TAACAAAATG AGGGCATAGG CTGCTGGCTT	420
GAACCATTCT TCAACGGTAG ACTCAAGGGC TTGTCTCGT TGGGTATCGT GGTTGTCGAC	480
AAAATCACAG ACTTGTCAAGG CTTGAGTTCA ACCAGGCT	518

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

CTCTGTCCTT TTACCTGAGA GTTTGAGCAG TTGCCTGCCT TGCCCCCTCG GTGCCTTTAC	60
GGTCTCTCCA GAGTTCCGTC CATTACAGT CATGGAAAAT CAAACGATTC CCCACTTCTA	120
TTAAACTTCA TTCGGTGTG GTATTTAATT GATTCTAATT TTACAAAAAA TGTTGGCTTT	180
TGTCATATGTG TTTATTAGTA AAAATTAGTT CAACAGTTT TACTTTATAA AGTCCAGAAC	240
ACTGCTATCC TTTAAAAGTG ACAATAGTCG CACCACTGCC TCCAGCATTT TGTGGGGCAT	300
AGCCGAAACT CTTGACATGT TTGTTCTTT GCAAGTATTT GGTAACCTCCT TCACGGATGA	360
CTCCTGTTCC GATACCATGG ATGATATCAA CTTGAGCCAT ATTGTTAAGC AAGGCTTGGT	420
CGAATGAAGG TATCTAGCTC ATTCACTGGCT TCTTCATAGC GCTTGCCCTCG AAGATTCACT	480
CTAGCTTGAG TCCTCGCCCA GAAGTTCG	508

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

CTCTTGGGCT CTCTTCTCAG CAACTTCCCT GCTTTCACCT TTGGTCTTGA TAGGTGANAA	60
CGTAATATNT CCAATCNNG TCATATTAGG AAANAGTTAA ATTGTTGGAA AACCATGCC	120
ATCTTCTCAC GCATGGGAAA CAGGTCAATT TTCTTGTCCG TAATATCGAC TCCCTCAAAG	180
ATAACCTTCC CCTTGGTTGC TTCCCTCCAAC AAATTCAAT AGCGAAGCAA GGTAGATTC	240
CCACTCCCTG AAGGACCGAT GATAACGACA ACTTCTCCTC TTTTAATCTC GAGGTTGATG	300
CCCTTCAATA CTTCATTCTT TCCAAAAGAT TTATGTAATT TTCAATTTTT ATCAAGGTTT	360
CTGTCATTAT TTCTTATC	378

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 741 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

CTGGCCAGCC AGATAAACCT CGATACGGCT TTCTGCTCGT TTGATGC GTT GCAAGAGTCC	60
GCCCCATACGG ACGTCAACTG TATCCAAACC AAAGACCTTG TTTTATTCA GCCAGTGGTG	120
ACTAAAGAGG GCATGGAAGT CTTCAATTG GCTTCTAAGT TCTGGTAATT CTTGTCTGGC	180
GATTGTTGT AAACTTCTT TATCATCCGC TTGGTAGGCA TGACGAATGC GTCGTCCCAC	240
ATCTACTTTG CTACTTAAAA TAGCATTCAA CTGGCCTGA GTTCAAAGA GATAAGCATA	300
GTTCAGCT TTTCTTAA TGTCAGCAAT AGTTCCCGCC GCCTGAGCGA AGTGTGGCTT	360
GTCCTGTTCA GGTGTCAATGT GTCGGTCAAG TATCGGACAG AGAACATCCT GATAAAAGAC	420
ATAGCGGTTG GGATTGATGC CACTGAGATT ACCTGGTAGG TCTGGTAAGA GTTGGCAAG	480
ATCAATCTGC ATAAAATCCT CAACCGTTAG ACCAGTATTG GTCTTAAAT GCGCAGACAA	540
ACTATCTAGG TCATTGCGAT AGATCAAGTT ATCGATAACCG TCGACCTCGA GGGGGGCCGT	600
ACCCAGATT GCAAGCTGG TAGGATAAAG AACTGGCAG TTTCACCA ACC ATTGTCTCCC	660
CAACCCGTTA CGATGACTTC TTTAATCTGA TTGGCACGGC AGGCTTATT AGCCTCGATA	720
GCCACTAGAC GGCTAAAATG G	741

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

AAACTCGATT TGAGAGAAAG TCCAATAAGT CTTTCCATAA TAAAACGCAT AGTAGCAAGA	60
GTTTCTACAC CCACATTAT GCGTTTTAT CATTGAAA TCTACTGCTA ATCAATGAAG	120
AAGCAAAGAT CAAACTAGGC AGCTAGTTAC AAGTTACGTA AGCGCGTCAT AACAAAGGTAT	180
CTATCCTAAT TCCCCAACTT CCAGTATACT AGATAAAAAAA TAATTATCGG AGGAAAGGTA	240
TTGTACTATG ATAATTCAAC TAAGTGATT AGGTCAAGTT CACCTTGTGTT GTGGCAAGAC	300
AGATATGAGG CAGGGAATAG ACTCATTAGC CTATGTAGTT AAAACCCACT TTGAATTGGA	360
TCCTTCTCC GGTCAAGCCT TTCTCTTTG TGGTGGACGT AAAGACCGCT TTAAAGCCCT	420
TTACTGGGAT GGTCAAGGAT TTTGGCTACT ATATAAACGC TTTGAGAACG GAAAATGAC	480
TTGACCAAGT ACAGAAAAGG ATGTCAAAGC TCTCACACCA GAACAAGTAG ACTGGCTTAT	540
GAAGGGCTTT TCTATCACTC CCCAAATATA GTGGATTAA ACTAGAATAG TACACCCCTA	600
CTTCTAAAAC ATTGTTAGAA ATCGATTTGA CTGTCTGAT CAATTGTCG TGTTCTTATT	660
TCATTTACT ATAGAATCCA TCTGAAAGCC GTTTATGATT TCTATTGAAA TGAAGACCGT	720
CCATTTAGT AGACTAAAGG ATTACTCAAAC TCTCGAGAA GGAAGACAGA TGAACCTGTT	780
TCTTATAAAA ATGTTGCTG AACTATTG CTTTTTCCA GAAATTAG AGGAAGAAAA	840
CTTTATGAGG AAAAAGGAGT TACTCAAATA ACAATTCAAGG ATTAAAAATA GACAGTTGAG	900
GAGCGGAAGG TATAAATTAA GTTGCTACT GTATAATGGA TTTAAATCAC TCAGCAGACA	960
GAACGAATAC TCTTCGAAAAA TCTCTCAGC CCACGTCAGC TTGCGCTTGC CGTAGATCCA	1020

TAGGGGACTG GACTTCATCA GTTCTATCAA CAACCTCAAA ACAGTGTTC GAGCTGACTT	1080
CGATCAATT TATCTGCACC TCAAAGCTGT ACTTTGAGCA AGCCTGACGA CTAGCTTCCT	1140
ATTTGATTTT CATTGAATAT CAGAAACTCA TTCTCCATCA AATAATTGCA CTGCGTCTAA	1200
TAATTTTG G TCTGGCACGG TGTCAGAAAT AAAGGTTGTG TATTTGGAGA GGGGATTAAT	1260
TTTAAAAAAAT CCAGTCTTGT AAAATTAGA ACTATCAATC AGTAAGATGG TTTCATGGGC	1320
TTTGTCAATA ATATTCTTT TTGAAATAG	1349

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

CTTTTTATA AGCAATTCAA TTTTATACTC ATCTGCTTTC AAAAAGCATT CTAGTCCATC	60
TCCGATTAAC GATGGACTTT ATCACCTCCT TCTCCAATCC TTGTATGACA TCTTGAAGTT	120
GATTCAATGAC ATCTTCCAAA ATTGAAAGG CTTTATTCTT AAATCCACGT TTACGAATCT	180
CTTTCCACAC TTGTTCAATG GGTTCATCT CTGGTGTGTA TGGAGGAATA AATGCAAAAC	240
CAATATTAGT CGGAATCTTT AAGACACTTG ATTTATGCCA TATAGCATTG TCCATAACGA	300
GTAAAAAATA ATCATCTGGA TAAGCTTG AAAGCTCTTC TAAAAGGCG TTCATCCACT	360
CAGTATTACA TCTACCAAGCT ATTAAGAAAA AATGATTCCG CCTGTTATGG GCATCAACAG	420
CTCCATAACA ATAGTGAAT TCTCGTATAT AGTGAATATG GACATGTGGA CCTACTCCTA	480
TTGGAGACCA ACAAGATCCC AGTTTACTGA TTCTACCGAA ACCAGCCTCA TCTTGGTACA	540
TCAAGCGAAC CTTATGAAAA CGTCTACTGG TTTAAATCGC TTTCTTGTCT TCTTGAATTG	600
AGATTTATT TTTAGACGCG ACAATGGTTT GAGCGTCTGC TTTCTTAGGA TGTTCTGGAC	660
GTGGCATAAT ATTCGCCAG CCATGGCGCT TCAACAGTTG ATAGAAGGCA TCACGTGTGT	720
AGGAACGACC TAACTCCATT TTATAAGCCT GAAATAAGGC ATCAATTGTA ACAAATTCTC	780
CTGCCTCTGT AGCCTTCAAA TGGCGGGCAA GAAATACTTT CTCTTCCTCA ACTGTCATAT	840
ATGCATGGTT ACACCACCC TTTCTGATA GAGTTGTTCA CATCTTATT CAAACTACTA	900
TAAAAGTTCT ATAATCTCTT TATAAGATTG GCCCATCAGA CGAAATATAA TAAATTGAAA	960
CTAGAATAGT ACACCTCTAC TTCTAAAACA TTGTTAGAAA TCGATTTGAC TGTCTGATC	1020
GATTGCCCC ATTCTTGTCTT CGTTTTACTA TAGAACGATT TGAAGGGCGTT TATGATATTG	1080
AGCTGTACGA GAGTCTTTA AAAGTGTGTTT GATGGCTTGG ATTTCTTCTT TAGTTGATTT	1140
CATATCACTA TTATATAATG CTTTTTGATC TTTAGTTAG TATTATCGTA GAAAATGGAC	1200
TAGGTGCTAT GGATACACCG GATGAGAATG GTTATGTAGC AGATGACTAT CGGATTACTT	1260
ACTTAGAGGC CCACATCAAG GCCATGCGAG ATGCCATTAA CCNAGACGGG GTTGACTTGCA	1320
TGGTTATAC GACTTGGGGC TGTATCGATC CAGTTTCAG	1359

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1082 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

CTAGTATTTC CGTTGTGNTT AGTTTGTCG CCTATGGAGT TATTGCCTAT GTGCAAGGTC	60
AGNTGGATAT TCTTCTAGTG ATTCTGGCCA TGATGGTGG TTTGCTCAGT TTCTTCATCT	120
TTAACCATAA GCCTGCTAAG ATCTTTATGG GTGATGTGGG AAGTTTGGCT TTAGGTGGAA	180
TGCTGGCAGC TATCTCTATG GCTCTCCACC AAGAATGGAC TCTCTTGATT ATCGGAATTG	240
TGTATGTTT TGAAACAACT TCTGTTATGA TGCAAGTCAG TTATTTCAAA CTGACAGGTG	300
GTAAACGTAT TTTCCGTATG ACGCCTGTAC ATCACCATTT TGAGCTTGGG GGATTGTCTG	360
GTAAAGGAAA TCCTTGAGC GAGTGGAAAGG TTGACTTCTT CTTTTGGGAA GTTGGGCTTC	420
TAGCAAGTCT CCTGACCTA GCAATTTAT ATTTGATGTA AGAATGGCAC CCTGATGTTT	480
TAGGGTGTAA TTGTGTTTAA ATACACAATG AAAATCAAAG AACAAACTAG AAAGCTAACT	540
TTAGGCTGCT CAAAACATAG TATATTGAAA CTAAAATAGT ACACCTCTAC TTCTAAAACA	600
TTGTTAGAAA TCGATTGAC TGTCTGATT ACGATTATC CTGTTCTTAT TTCATTTTAC	660
TATACCATCA ATAAGTGTG AAAAGATCGT TGACAGAACT GACCAAGCCA GATCATCTT	720
GTAACCACCT TGAGCTTGTA GCATATTTGT TAATTGAGCA AAGGCGCTAG AAGAGTTTGC	780
TGGGTCAGCA GTTGCAGATT TTCCCTTTAG TTCAGGTTTG AGAAGGTCGC TATATCCTTC	840
GATGTTCATG CCTTAGTTA AATCAGGGTG GACGATTAAA ACACTACCAT CTAGTGTATA	900
AGGAGTAGAG AAGCCAGTTG TGTTTGATA TTCTTGATA ACATTATCAT TTTCTTTGAA	960
AATATAGTT TCAAAGAGTT CTCCGTGGGT AGCATATTGT GTTATAAGAA CCACCAAAGA	1020
TAACATCAGC TACAGGAAC TCTTTTCTG ACCTAGTTT TTGAAAAGTT CTCCAGTACC	1080
AG	1082

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

CTGGACTTGA TAGGCATCTT TGTAATCCTC TAAAGCCTCT TTCATCAAGG CACTACCAAT	60
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TCCTTGACGC	TGATAGATTG	GTAAAACGAT	TAATCCTGA	ACCAATACTG	ATGAGAATCC	120
ATCTCCAACC	AAACGAATCA	AGCCCACCCAC	AGCATCACCA	TCAAGTGCCA	CATAAATTAC	180
TAATGAATGA	GATAAGGCCT	GCTCCAGCAT	CTCTGGTTGA	TGGGTATAAT	TAGTCAAACC	240
GACAGCCTGA	TAGACATGTA	AAACATCCTC	TAGCTTGACA	ATTTCTTGCT	TTTTAATAGT	300
AATCATCTCA	ACACCTCTTA	AAGTTCTCTC	AAGCTTTGT	ACTGCTGTCC	ATTTTTATCA	360
AAATTTTCAG	GACGCAACCA	TGTTTCCAAA	CGATCTTGA	CTTTGGGCCA	GTCCTTATCA	420
ATCATAGACA	ACCAATCCAT	ATCTCTCGTA	CGCCCCTTAT	AAACCACTGC	CTGACGGAAAG	480
GTTCCTTCAT	AAATAAAGCC	CAAACGCTCC	GCAGCACGTC	TGGATGGCAG	GTAAAGAGCA	540
TCGCATTTC	ACTCATAACG	ACGATAGTTA	AGCTCTTCAA	AGACATAGCG	AGCCAGTAGA	600
TACTGGGCTT	CTGTCCTTAT	CCGTGTCCCC	CTGAGTTTG	GAGAAAAAGT	GACAGCTCCC	660
ACTTCTATTA	CTCCGTTACT	GGTCAATAACG	CATGAGAGAA	AAATCCCAA	AGCCTTACCA	720
GTTGCCTTGT	CTATGTAGTA	AAAACGGTCC	TTACGAGCCA	ACATCTGACT	ACTATAGTAG	780
ATTGAAACTA	GAATAATATA	CCTCTACTTC	AAAAATATTG	TTAGAAATCG	ATTTGACTTC	840
CCTGATCGAT	TCGTCCTTATT	CTTATTTCAT	TTAATATATAA	TTGATAGTGG	TCGCCCCAGC	900
CAGATACCTT	ATCTGCTATC	CATTTAGGAA	CCCCTAACTT	AAGCAATCCC	CATAATCGTC	960
TCGATTTCTT	CTTCCATTGC	TTCCAGATAA	TCACTCGTAG	GCGAGTACGC	AAGCGCTCAT	1020
CTATGTTAGT	GACTATACTT	TTCATATTTA	TAATTCAATT	CTTTCGTTTC	ACTCAAGGCA	1080
CAACACAGAA	TGAAAAAGTG	TTGTGATCTT	TATTTTGT	TATAATAATA	GTGAGAAAGC	1140
CTATCACTAC	TACAAATCAC	GGGGAGGTGA	ATAAGTGAGT	GGTACAGCCA	CTACCTCGCA	1200
TATTTTGTCA	CATCATTAA	CGGTACATAA	TAAGTTGTAC	CATCTGAATA	AGTTGCTACA	1260
ATATCATTG	CATGCTCTCC	TTCACCTTA	GCAAAGGTTG	GAG		1303

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

CTCTTCAATC	AACTCACGCT	TTAGGGCTTC	CTGATGATT	TCACCTGCTT	CAATTCTCC	60
ACATGGTAGG	AACCAAGCAC	CATTTGGTTC	TTGAACAAGA	ACAATTGTT	TTTGTTCAGG	120
ATTAGGGATA	ACTGCATATA	CGCCATAGCG	AGCAATATAG	TCTGTATTG	CTTTTTCTC	180
CGAAAGTTGG	GTTTGCCATT	GCATTTCC	CATTATCTAG	TATCGTTATT	ATTATAGTGA	240
AATGAACCAA	AAATAGTACA	CAATGTGGTA	TAATCTTTT	ATGGCATATT	CAATAGATT	300
TCGTAAAAAA	GTTCTCTCTT	ATTGTGAGCG	AACAGGTAGT	ATAACAGAAAG	CATCACACGT	360
TTTCCAATC	TCACGTAATA	CCATTTATGG	CTGGTAAAG	CTAAAGAGA	AAACAGGAGA	420
GCTAAACAC	CAAGTAAAAG	GAACAAAACC	AAGAAAAGTT	GATAGAGATA	GACTTAAAAA	480
CTATCTTACT	GACAATCCAG	ACGCTTATT	GACTGAAATA	GCTTCTGAAT	TTGGCTGTCA	540
TCCAACCTACC	ATCCACTATG	CACTCAAAGC	TATGGGCTAC	ACTCGAAAAA	AAGAACACACA	600

CCTACTATGA ACAAGACCCA GAAAAAGTAG CCTTATTCT TAAGAATTT ANTAGTTAA	660
AGCACCTAGC ACAGGTCTAA CAAATGGTGA ATTAATCGCT CCAATGACTT AGCAAGAGAT	720
GATGACGAGC GACTTTTGT AAGTATGGTT TCAGAAGTTT CTCTTACCAA CATTAACCAC	780
ACCATCGGTT ATTATAGTGA AATGAAATAA GAACAGGACN AATCGATCAG GACAGTAAAA	840
TCGAATTCTA ACAATGTTT AGAAGTAGAG GTGTACTATT CTAGTTCAA TCTACTATAT	900
TAATGGACAA TGCAAGATTC CATAGAATGG GTAAGCTAGA GTTCTTATGT GAAGAGTTG	960
GGCATAAACT TTTACCTTT CCTCCCTACT CATCTTAGTA TAGAAAAGTG AATCTAAAAT	1020
AGTACATAAC TGCTTCTAAA ACATTCTTAT AAATTGATTT AAATTCTCAA ATCATATTAT	1080
TCAGTTCTTA TTTCATTGCT CTCTACAATC CTGTTGAGAA GACACGTGTT CATATCAAAA	1140
AGGTATTGGC AAGTTGCAAT ACCTTTTAC AAGGTTCTTT TGTCTTATTT TTGTTTCAAC	1200
TGACTATATC TCCTATGGTT CTAGTTCAGA AGGCTAGGCT ATAATTATGA TTGATAAGAA	1260
GTATCATTCC AAGTATTGAG AGTGAATGTT TCAAAATCAT GGGTTTCTAT AATGGTCAGG	1320
CTGGCATTG CTAGACCGCC ATCTTACGA AGAAGTGGTT CTTTATAGCC TAGGAGAGTA	1380
CGAAGACTGG CAGTAAGATT GGGCCCGTGT CCGACAATTA GAATACGCTC AGCTGGACTA	1440
TCTTTTAATG ATTTGATAAA TTGGATGGTC CGCTGAGTTG TACTATAGAG GGATTGGCT	1500
CCGAACATTC GAGTGTCAA TTGAGCAAGA TTTGAACGAA AAGCCTGGAT TTGTTGGGG	1560
TAAATAG	1567

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

CTGTTCCAT AGCATGACTT CTGTACTAGA CTTCTTTTC CGAATAAATA GATAGAACCA	60
CAGAACCTAG TAAACCTAGA ATTAAAATTA TGGTATAATA TTAGCAATAA AAGAAATCTG	120
GAGGATTAGA ATCATGGTAT CAACGAAAAC ACAAAATTGCT GGTTTGAGT TTGACAATTG	180
CTTGATGAAT GCAGCAGGTG TGGCTTGTAT GACGATAGAG GAGTTAGAAG AGTCAAAAAA	240
CTCAGCGGCA GGAACCTTG TTACTAAGAC AGCGACCTTG GACTTCCGTC AGGGAAATCC	300
TGAGCCACGC TACCAAGATG TTCCACTTGG TTCCATCAAC TCTATGGGCT TGCCAAATAA	360
TGGCTTAGAC TATTATTGAG ATTATCTTT AGATTGAG GAAAAAGAGT CGAACCGAAC	420
TTTCTTCTTA TCTCTGGTCG GCATGTCTCC AGAGAAACCC ATACTATTG GAAAAAGTC	480
CAGAGA	486

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 814 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

CTCTATCAGG AAAGTTAAAT TAATTTATAG AAATATTTA GTATTTAAC CCTACTGTTA	60
TAGATTCAAT ACACTATATA TGTGTTGTC TGATAAAAAT TTCTACTCTT TTTGATTTA	120
AATAAGTATT AGTTTACATT ATGGTGTGAA TTGGGTTTGA TATCTCTTT GAGGAAGTTG	180
CCTTAGATT TTCTGATTGT GTTTTATTGT ACAGTGTATC TTGCTTGTGTT TGAACAGAAT	240
TTTTTATGAC ATTTGTCATA TTTTCTAGTG ACAGAAGCTT CTGCCTCCCTC TGATTTTAAA	300
AGACTATAAT TGTAGTATGA AATGGGGAA GAAGAGATGA GAAATAAAAT GATTATCGCA	360
GTAAGTTTAG TAGTAGCAGG AGTTATGACC TATCTCATGT TTTCGGGATT GGATGAGAAT	420
TTCTACCATT TTCCTGGGA GGTCTTGCT GGCTTGAA TCATCTCTT GGCTTGTCCA	480
GAGAAGGTTT GAAATTAGTA AGAGATGTGA AAAAGGAGTT TGAAAAATGA AAAAAGCAAC	540
TATCTATTTC TTTATCGGCC TGTCACTCTT GGTATGGTTG GTAGAAATGT TTACAGGTTG	600
GTTTGCTCAA ACCTTCCTTC ACCAGTTCAT CCGTGGTGCA TGGGGATTAG GATTTATGAT	660
TTTTATCGCC TTTCCGATGG GAAAGGAGTT GCTGGAAGGA GAATATCATG AACATGATTA	720
AGGTTCAAGG ACTACATAAA AATATTAAGG GCAAGGCTAT TTCAAAGGAT ATTCCTTTG	780
AAAGTAGCAGA AGGTGAATGC GTTGCCTTGA TTGG	814

(2) INFORMATION FOR SEQ ID NO:217:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1319 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

CTTGGTACGA CCGTATGGGT GGTCACTGAA AGTGGGAAAC TTCCAAGATG GGCACTGTGT	60
ACGGATCCCC GTAAACTGTC GCANAAGAAC TGAAGATGAT GTTTTTACAG TTGTTTCTT	120
CCATGGCTTT CAAAAGGCTG ACAGTTCCAG CGATATTGTT GTCATAGTAG GCAAGAGGGA	180
TACGTGTTGA TTCGCCAACA GCCTCAAAC CAGCAAAGTG AATGACACCA GTCAGTTCTT	240
CCTGCTTGAA AATATCTCTG AGGGTATCTG TGTACACNAAT ATCTGCCTCA TAGAAAGGAA	300
TCTCAACTCC TGTGATTCTT TCAACAACCTT CTAACACTCTT ACNATTGCTA TTGACAAGAT	360
TATCCACCAAC AACAACTTGA TGGCCTGCTT GGATCAATTCAATAACAGTG TGGGTTCCAA	420
TAAAACCGGC ACCACCAGTT ACCAAAATCT TTTCTTGCAT CTTTTTCCCT CGATTCTCAG	480
ATTATTTTTT CTTATTTAA CCATTTTGA CAGGAATGT CATTGCCAC CTTAAACTAC	540

CTGATAAAAAT	TTCAGTAAAAA	TGCTTATACT	CTTGGAAAAT	CCAATTCAAA	CCACGTCAAC	600
GTCGCCCTGC	CATGGGTATG	GTTACTGACT	TCGTCAGTTC	TATCCACAAAC	CTCAAAGCAG	660
CGCTTGAGT	AACCCGCGGC	TAGTTCTNTA	GTTTGGTCTT	TGATTTCAT	TGAGTATTAT	720
TCGCTTTTA	CTCGTTGAC	ATAGTTTCA	ATTGGTAGT	TTTCAGGGTC	CAAGGTCAAC	780
TCCTTGCTT	GGATCAGTTG	AGCTAAATGG	TAACCAATAA	TAGGACCAGT	TGTGAGGCCT	840
GATGAACCTA	GTCCACTGGC	TGCATAGACA	CCAGTTAAGT	CAGGCACCTG	CCCAAAGAAA	900
GGAGAGAAAT	CACTGGTGT	GGCACGGATT	CCAACACGCT	CAGATTTGA	AGTAGCTTC	960
GCCAAAATCA	GATAGTGAGT	CAAGGTGGCC	TCCTCCATTT	GTTGGAGCAA	GGTTTCATCT	1020
ACCGTCAAAT	CAAATCCCAT	GTCATTTTCG	TGGGTAGCGC	CTAAGGACAA	TTTCCCACCT	1080
GCAAAAGGAA	TCAAATCCC	CTCCCCTTCT	GGCATGACAA	CAGGGTAAGC	TTCCATGTCT	1140
TGGACCAGCT	GATAATCTCG	TAGTTGTCCT	TTTGAGGAC	GAACATCTAC	TTCATAACCC	1200
AAGGGTTCTA	ACATGTCCCC	CAACCAAGCT	CCNGTCGCCA	AAATAACCTG	CTCAAACCTCC	1260
TCTTCACCAA	TCTGGTAGCC	TGATGCTAAC	GGTGTCAAGAG	TCACTTTTC	TTTGACCAG	1319

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

CTCAAAATAC	TGTTTGAGG	TTGCAGATGG	AAGCTGACGC	GGTTTAAAGA	GATTTTCGAA	60
GAGTATAAAC	TGCTTATAAA	ATAAAAAGGA	GCCCTGATGG	AACACATTAT	TTATCAGTTT	120
GAAGAGGACT	TGGCAATCCT	TACCTTGAAC	CGTCCTGAGG	TCGCAAATGG	TTTCATATT	180
CCCATGTGTG	AGGAGATTTT	AGAACGCTCG	ACTTTGGCAG	AAGAAAATCC	AGCTGTGCAT	240
TTTATCTTAA	TCAATGCCAA	TGGAAAGGTC	TTCTCAGTTG	GGGGAGATT	GGTAGAGATG	300
AAGCGGGCAG	TGGATGAGGA	TGATATTCCA	TCATTGACAA	AAATCGCAGA	GTTGGTCAAT	360
ACGATTCTT	ATAAAATCAA	GCAAATAGCC	AAACCTGTTT	TTAATGGAAG	TTGACGGTG	420
TGTTGCAGGT	GCCGCAGCGA	ATATGGCTGT	TGCGGCAGAT	TTCTGTTGG	CGACGGATAA	480
GGCTAAGTTT	ATCCCAAGCC	CTTGTGTTGGT	GTGGTTGGCT	CCAGATTCCA	GGGG	534

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 784 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

CTGCAGCCGG AAGTTATCTG GTTACAAAAA ATCGCCAAAC CATCACAGAT GAAAGTCCTG	60
AATAACCACTG ACCGCGTTCA AGCTATCAAG GACGATGTGG ATATTATCCA AAACAGCCTG	120
CAAATCATTA ACCAGCAAAA AGAACTTATC AAGGAATACC AAGAAGACTT GACTTACAAG	180
TTTAAGGTCT TGGAAAAGGA TATCCAAACT AGGACTAGCT GTGATAAAAG AAATGCAGGG	240
AACTGAAGAT AAGTAAAAG AGCCCGACGG CTCTTTTTA AAACGTAAAC AAGTTATAGT	300
GAATTGAATT TAGAATAGCA CATCATAGTT TCTAAAGCAT TGTTAGAGAT TACTTTAAAAA	360
TCCTCTTATC AATTGTTCA TATTCTATTT CAATCTACTA TATATATCCC ATCAACTATG	420
CATCATAATT TAGGTAACTC ATACTCAATA AAAATCAAAA AGCAAACCTAG AAAGCTAGGC	480
ACAGACTGCT CAAAACACCG TTTTAAGGTT GTGGATAGAA CTGACGAAAGT CAGTAACCAT	540
ACCCATGACA AGCCGACGCT GACGTGGTTT GAAGAAATT TTGAAGAGTA TCATTCACCA	600
TTTCACAACAACT AAATCGAAGA CTTCTGCCG TAATGAAAAC ACCTGAAACA GCTTGGTTTC	660
AGCTGTCCGG AAACTTAACG ACTTAGGTTCA AAAGTTAGG TATGGAACCTT CGAAGGAGGT	720
CGCTACCGTC CGTCATTACT TAGNGAAGNC TTAAAAAAATC TATAAAAGTAA AAAGAGCCCCG	780
ACAG	784

(2) INFORMATION FOR SEQ ID NO: 220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 962 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

CTACTCGTT TAGTATAGTA AACTGAATCT AGACTAGCAC AATGCNGCTT CTANAGCGTT	60
TCGAAACTAG AATAGGACAA CATAACTGCT AAAAGATTTC TATAAATTCA TTTGATTTTC	120
CTAATCAATT TGTTCGTATC CTANTTCACT CCACTATAAA ATATTCTTAT CAATTGATTT	180
GNATGCCAAA ATTCCATCGT TCAGGTCTTA TTTCATTNNG CTNTAAAAAA CTCTCCTGGG	240
NAATCCAGG AGAGNATGAT TACNTATTG AACTTGAATC CTTCGTANAT AAGCTCTGTT	300
TTTGGATTTT GTTTCTTAAT CTGTTGGCA AGTGCCTTCA TCATAGAAAT AGGACCACAC	360
ATATAGACGG TTGCATGTTC GGGCACTTTT TTTGTCAAA ATTAAGATAG CCGTCTTTCG	420
TACTGTCGAT TAGATGGAGT TCAAAATTAG GATTTTCTG AGCATAGTTA CGGAGTAAAT	480
CTAGGTAGAC TGCATTTCA TCTCCACCGA AGCTATAGTA GAAGTGAACC TGTTTATCTA	540
AAATAGGATG TTCACGGATG TAAGAGATGA AGGGGGTGAT CCCAATACCT CCAGCAATCC	600
AAACCTGATT TTCTCGTCCT TCTTCTATGA TCATGTGTCC GTAAGCTCTG TCTAGGGTTA	660
CTTTGCTGCC GGCTTGAAGA TTATCATAGA TATTTCCTGG TATGGTCGCC TGAATTTTA	720
ACAGTAAAGT TAAAGAGTTT GAACCCATGA ACTCCCTGAG AATAGAAAAG GGATGCCGGA	780

ACCACTTCA AAGCCTTCTT GGAAAATCTT TAGAAAGGCA AATTGTCCCTG ATTGATAGTT	840
GAAAGGTCTG CTAAGATGGA TTTGAATTC TCTAGTATCG TGATTTAAGC GTTGAGATG	900
GGTAATTTTC CCTAGATAGG GGAAGGAAAT CTTTGATAT AGAAAATGA TATAAAAACC	960
AG	962

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 910 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

CTCTTCCAC TATTATAACA CGAAAGAAAG AATTGTCAGG GAACTGTACA GATTCTTTT	60
CTATCTATTT ATAACATCAAAT GAAAATCAAA GAGCAAACTA GGAAACTAGC CGCAGGCTGT	120
AATTGAGTAC GGCAAGGCAGA CGTTGACGCG ATTTGAATTG GATTTTCGCA GAGTATTATT	180
CGTAAAAAAT CTCAAAAAGC CTACCTTTCG GTAGACTTAG TTTGTTTCTA TTCTAACCGG	240
CACTCTCCA AAATTTGCT CTGCTATACT TGGCTTCCT AGTTGGTAAA TCTGGTCAAC	300
CTTTTGAGTC ATAGCATCCC AAGGTTCTT GCCAATTCTGG CTGACTAGAT TGACCTGTCC	360
TTTCAGAGAC TTGAGATGTT GCCTGCCTTT TTCAGTAAAT CCAAGGACAT GAATGGCTTC	420
TGGCAAGTCA CTTTCTCTAG CCTGCATCAA AATATAGGTC AATAGGCGTC TGACACGCGC	480
CTTGGTGTAA CGTTGGTAG TCACTAACCTC GACCAATTCT TCCACAGACT GGGCTGTTTT	540
AATAGCTTCT TTAATGCGCA CAGCCATTTC TTGATTGACC TGATAGATGG TGGTTAGGTC	600
GGGATTGAC AAGATTGAT AGCGGAGCAA GGGAAAATAG TCTTCCCAGA TCACCTTACT	660
GGCTTGCTCA AATAGGCCAA CAGAAGGCAT AAAACGTTCT AAGAAATCTT GGTCCTTCTG	720
ATGTTGACGG AGGGCTGTCG CCGAGGCAA GTCCACATCT TTATTACAG AATGGTAACC	780
TGCCCCCTGA CGCTGAATCG GATGCAGCTT GATATTCCGT CCTGCAACCG CCTTGGCATA	840
GGCCAAAACA AAGAACATGA TTGGGGTGTAA TTACCTGAAA AATCAAGACC AGCAAATTCC	900
TTCCACATAG	910

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 866 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

CGCCAAGTCA	TCCAACAAGT	CCAGAACGGT	TCTGGGGCTT	GGGATCCTCA	GTCGCTGGAG	60
ATAACTCCTT	TGGGCTTGTT	CATCATGTAG	TAGACAAACT	CTTCATACTC	CAACACTTGC	120
CCATCAAAAG	CGAATCTCAT	CTATTTTTC	ATCAATCTGC	AATTAGCTG	ATTTTCTTT	180
TTTACCATT	ACAGTCACGC	GCCCAGCCTT	GAGCAAGTTT	TTGACCTCAG	TCCGACTTCC	240
CACCGCACAG	GCAACTAAAA	ATTTATCTAA	TCTCATAGAA	CTATTATATC	ATATCAAAG	300
GAGGCTGGTA	CAATGACCAA	CCTCCTTTTC	GTTCATACT	CTTCAAAAAT	CTCTCAAAC	360
CGCGTCAACG	TCGCCTTGCC	GTATATATGT	TACTGACTTC	GTCAGTTCTA	TCTGCAACCT	420
CAAAGCAGTG	CTTGAGCAA	CCTGCGGCTA	GTTCCTAGT	TTGCTCTTG	ATTTCATTG	480
AGTATCAGAT	TTAGGAAATT	AACTCCTCG	TCTCCAAAAA	ATAGCTAAGA	CAATCATGGC	540
ACCTAAAACA	GCTGGGATAA	TAGCTGTTCC	TGATAAAAAT	GGCCCCAAG	TTCCAAAGAG	600
CAAGTGACCT	AGAAAGGCTC	CGATCCAACC	GAGAACATT	TTTCCAAAAC	ATCCCATTG	660
CTCTCCACGA	TTGGTCATAG	CACCTGCTAA	AAATCCCACT	AGGAGACCAA	CGAACATACT	720
TCCTAACATA	TTATCTCCTT	AATTTGCCCA	ATTCCATTAA	CGGAAAAGAA	CTACTCGCGT	780
TCCATCCTCA	CGAATACCAT	CGATATCCAT	TTGGTTAGAA	CCAATCATAA	AGTATACGTG	840
AACATCTGAA	CGGTTAAGCC	CTGCGAG				866

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

CTTCAGGATG	TGGGAAAACG	ACCCTTCTTC	GTATGATTGC	AGGTTCAAC	AGTATCAAAG	60
ATGGAGAATT	TTACTTCGAT	GATACAAAAAA	TCAATAATAT	GGAACCCAGC	AAACGCAATA	120
TCGGGCTGGT	TTTCCAAAAC	TACGCTATT	TCCCACATT	GACTGTCCGA	GACAACGTTG	180
CTTTTGGTCT	TATGCAAAAG	AAGGTTCCAA	AAGAAGAATT	GATTCAACAG	ACCAACAAAGT	240
ATCTTGGACT	CATGCAAATT	GCTCAATATG	CGGATCGAAA	GCCCGATAAA	CTCAGTGGTG	300
GACAACAACA	ACGTGTCACC	TTGGCATGCG	TCTTAGCGGT	TAATCCAAGT	GTTCTCCTCC	360
ATGGACGAAG	CCACTTAGTA	ATCTGGAGGC	CAAACCTCGC	TTGGATATGC	GTTCAAGGCC	420
ATCCCAGAGAA	ATCCAACCAAC	GAAGTTGGGG	AATTACAAC	GTTTATGTAA	CCCACGACCA	480
AGAAGGAGCC	ATGGCTATTT	CAGACCAAAT	TGCCTGTTAT	GAAAGATGGG	GTGATCCAAC	540
AAATCGGCCG	ACCAAAAGAA	CTGTATCATA	AACCAGCTAA	TGAGTTAGTG	GCAACCTTTA	600
TCGGACGCAC	AAATATTATC	CCTGCCAATC	TTGAAAAACG	GAGCGACGGC	GNTTATATCG	660
TCTNTTCAGA	TGGANANGCC	CTTCGAATGA	TAG			693

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

Met	Ser	Met	Phe	Thr	Met	Val	Lys	Met	Asn	Pro	Leu	Arg	Gly	Leu	Ile
1					5						10				15
Cys	Asn	Leu	Lys	Gly	Asn	Lys	Ile	Thr	Ala	Leu	Ile	Gly	Pro	Ser	Gly
					20					25					30
Ser	Gly	Lys	Ser	Thr	Tyr	Leu	Arg	Ser	Leu	Asn	Arg	Met	Asn	Asp	Thr
					35			40				45			
Ile	Asp	Ile	Ala	Lys	Val	Thr	Gly	Gln	Ile	Leu	Tyr	Arg	Gly	Ile	Asp
					50			55			60				
Val	Asn	Arg	Pro	Glu	Ile	Asn	Val	Tyr	Glu	Met	Arg	Lys	His	Ile	Gly
					65		70			75				80	
Met	Val	Phe	Gln	Arg	Pro	Asn	Pro	Phe	Ala	Lys	Ser	Ile	Tyr	Arg	Asn
					85				90				95		
Ile	Thr	Phe	Ala	His	Glu	Arg	Ala	Gly	Val	Lys	Asp	Lys	Gln	Val	Leu
					100				105				110		
Asp	Glu	Ile	Val	Glu	Thr	Ser	Leu	Ser	Gln	Ala	Ala	Leu	Trp	Asp	Gln
					115			120				125			
Val	Lys	Asp	Asp	Leu	His	Lys	Ser	Ala	Leu	Thr	Leu	Ser	Gly	Gly	Gln
					130			135			140				
Gln	Gln	Arg	Leu	Cys	Ile	Ala	Arg	Ala	Ile	Ser	Val	Lys	Pro	Asp	Ile
					145		150			155				160	
Leu	Leu	Met	Asp	Glu	Pro	Ser	Leu	Ser	Leu	Gly	Ser	Asp	Cys	Asp	His
					165				170				175		
Ala	Thr	Arg	Arg	Asp	His	Val									
					180										

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

Met Ile Lys Ile Ser Asn Leu Ser Lys Ser Phe Ser Gly Gln Thr Val
1 5 10 15
Leu Asp His Leu Asn Leu Asp Ile Gln Lys Gly Glu Val Val Ala Leu
20 25 30
Ile Gly Ser Ser Gly Ala Gly Lys Ser Thr Phe Leu Arg Ser Leu Asn
35 40 45
Tyr Leu Glu Thr Pro Asp Ser Gly Ser Ile Gln Ile Asp Gly Phe Ser
50 55 60
Val Asp Phe Ser Lys Ile Thr Gln Glu Glu Ile Leu Ala Leu Arg Arg
65 70 75 80
Lys Leu Ser Met Val Phe Gln Gln Phe Asn Leu Phe Glu Arg Arg Thr
85 90 95
Ala Leu Asp Asn Val Lys Glu Gly Leu Val Val Val Lys Lys Leu Ser
100 105 110
Asp Gln Glu Ala Thr Lys Ile Ala Lys Glu Glu Leu Ala Lys Val Gly
115 120 125
Leu Ser Asp Arg Glu Asn His Tyr Pro Arg His Leu Ser Gly Gly Gln
130 135 140
Lys Gln Arg Val Ala Leu Ala Arg Ala Leu Ala Met Lys Pro Asp Val
145 150 155 160
Leu Leu Leu Asp Glu Pro Thr Ser Ala Leu Asp Pro Glu Leu Val Gly
165 170 175
Glu Val Glu Lys Ser Ile Ala Asp Ala Ala Lys Ser Gly Gln Thr Met
180 185 190
Ile Leu Val Ser His Asp Met Pro Phe Val Ala Gln Val Ala Asp Lys
195 200 205
Ile Leu Phe Leu Asp Lys Gly Lys Ile Ile Glu Ser Gly Thr Pro Asp
210 215 220
Glu Ile Ile His Thr Pro Lys Glu Glu Arg Thr Lys Glu Phe Phe Thr
225 230 235 240
Ser Tyr Lys Arg Thr Tyr Ile
245

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

Met	Phe	Ser	Leu	Arg	Ser	Val	Phe	Asp	Gly	Ile	Pro	Arg	Ile	Val	Gln
1							5			10					15
Gln	Leu	Pro	Thr	Thr	Ile	Met	Leu	Thr	Ile	Gly	Gly	Ala	Leu	Phe	Gly
						20			25						30
Leu	Val	Leu	Ala	Leu	Leu	Phe	Ala	Ile	Val	Lys	Ile	Asn	Arg	Val	Lys
						35			40						45
Ile	Leu	Tyr	Pro	Leu	Gln	Ala	Phe	Phe	Val	Ser	Phe	Leu	Lys	Gly	Thr
						50			55						60
Pro	Ile	Leu	Val	Gln	Leu	Met	Leu	Thr	Tyr	Tyr	Gly	Ile	Pro	Leu	Ala
	65					70				75					80
Leu	Lys	Ala	Leu	Asn	Gln	Gln	Trp	Gly	Thr	Gly	Leu	Asn	Ile	Asn	Ala
						85			90						95
Ile	Pro	Ala	Ala	Ala	Phe	Ala	Ile	Val	Ala	Phe	Ala	Phe	Asn	Glu	Ala
						100			105						110
Ala	Tyr	Ala	Ser	Glu	Thr	Ile	Arg	Ala	Ala	Ile	Leu	Ser	Val	Asn	Pro
						115			120						125
Gly	Glu	Ile	Glu	Ala	Ala	Arg	Ser	Leu	Gly	Met	Thr	Arg	Ala	Gln	Val
						130			135						140
Tyr	Arg	Arg	Val	Ile	Ile	Pro	Asn	Ala	Ala	Val	Val	Ala	Thr	Pro	Thr
	145					150				155					160
Leu	Ile	Asn	Ser	Leu	Ile	Gly	Leu	Thr	Lys	Gly	Thr	Ser	Leu	Ala	Phe
						165			170						175
Ser	Ala	Gly	Val	Val	Glu	Val	Phe	Ala	Gln	Ala	Gln	Ile	Leu	Gly	Gly
						180			185						190
Ala	Asp	Tyr	Arg	Tyr	Phe	Glu	Arg	Phe	Ile	Ser	Val	Ala	Leu	Val	Tyr
						195			200						205
Trp	Val	Val	Asn	Ile	Gly	Ile	Glu	Ser	Leu	Gly	Arg	Phe	Ile	Glu	Arg
						210			215						220
Lys	Met	Ala	Ile	Ser	Ala	Pro	Asp	Thr	Val	Gln	Thr	Asp	Val	Lys	Gly
	225					230				235					240
Asp	Leu	Arg													

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

Met	Tyr	Arg	Ile	Asp	Asp	Asp	Glu	Gln	Phe	Val	Leu	Asp	Phe	Leu	Lys
1				5					10				15		
Gin	Glu	Lys	Val	Leu	Leu	Val	His	Gly	Arg	Gly	Phe	Asn	Trp	Gln	Glu
			20				25				30				
Pro	Asp	His	Phe	Arg	Ile	Val	Tyr	Leu	Pro	Arg	Val	Asp	Glu	Leu	Ala
			35				40				45				
Gln	Ile	Gln	Glu	Lys	Met	Thr	Arg	Phe	Leu	Lys	Gln	Tyr	Arg	Arg	
			50				55				60				

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

Met	Asn	Asp	Glu	Ala	Ser	Lys	Gln	Leu	Thr	Asp	Ala	Arg	Phe	Lys	Arg
1				5					10				15		
Leu	Val	Gly	Val	Gln	Arg	Thr	Thr	Phe	Glu	Glu	Ile	Leu	Ala	Val	Leu
	20					25					30				
Lys	Thr	Ala	Tyr	Gln	Leu	Lys	His	Ala	Lys	Gly	Gly	Arg	Lys	Pro	Lys
	35					40					45				
Leu	Ser	Leu	Glu	Asp	Leu	Leu	Met	Ala	Thr	Leu	Gln	Tyr	Val	Arg	Glu
	50				55			60							
Tyr	Arg	Thr	Tyr	Glu	Gln	Ile	Ala	Ala	Asp	Phe	Gly	Ile	His	Glu	Ser
	65					70			75			80			
Asn	Leu	Ile	Arg	Arg	Ser	Gln	Trp	Val	Glu	Val	Thr	Leu	Val	Gln	Ser
					85			90			95				
Gly	Val	Thr	Ile	Ser	Arg	Thr	Pro	Leu	Ser	Ser	Glu	Asp	Thr	Val	Met
			100				105				110				
Ile	Asp	Ala	Thr	Glu	Val	Gln	Ile	Asn	Arg	Pro	Lys	Lys	Arg	Ile	Ser
					115			120			125				

Glu Ser Phe Trp

130

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

Met	Arg	Arg	Lys	Tyr	Lys	Ser	Ile	Ala	Leu	Lys	Lys	Glu	Leu	Ala	Asn
1					5					10					15
His	Ser	Gly	Lys	Lys	Lys	Phe	His	Ala	Met	Lys	Ala	Gln	Ala	Ile	Val
							20			25					30
Thr	Ser	Gln	Gly	Arg	Ile	Val	Ser	Leu	Asp	Ile	Ala	Val	Asn	Tyr	Ser
					35				40					45	
His	Asp	Met	Lys	Leu	Phe	Lys	Met	Ser	Cys	Arg	Asn	Ile	Gly	Gln	Ala
						50			55					60	
Gly	Lys	Ile	Leu	Ala	Asp	Ser	Gly	Tyr	Gln	Gly	Pro	Met	Lys	Ile	Tyr
					65			70			75				80
Pro	Gln	Ala	Gln	Thr	Pro	Arg	Lys	Ser	Ser	Lys	Leu	Lys	Pro	Leu	Ile
					85				90					95	
Ala	Glu	Asp	Lys	Ala	Tyr	Asn	His	Ala	Leu	Ser	Lys	Glu	Arg	Ser	Lys
						100			105					110	
Val	Glu	Asn	Ile	Phe	Ala	Lys	Val	Lys	Thr	Phe	Lys	Met	Phe	Ser	Thr
						115			120					125	
Thr	Tyr	Arg	Asn	His	Arg	Lys	Arg	Phe	Gly	Leu	Arg	Met	Asn	Leu	Ile
						130			135					140	
Ala	Gly	Ile	Ile	Asn	Tyr	Glu	Leu	Gly	Phe						
						145			150						

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

Met Val Ser Ser Ser Gly Ser Glu Phe Gln Ser Gly Trp Gln Glu His
1 5 10 15
Gln Leu Ile Ala Glu Lys Val Ser Lys Thr Leu Asp Lys Thr Phe Asp
20 25 30
Lys Asp Val Arg Lys Ile Pro Thr Ser Pro Val Leu Ser Lys Ile Cys
35 40 45
Arg

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

Met Ile Lys Ile Leu Ala Ala Cys Gly Ala Gly Val Asn Ser Ser His
1 5 10 15
Gln Ile Lys Ser Ala Leu Glu Glu Glu Leu Ser Asn Arg Gly Tyr Asp
20 25 30
Val His Cys Asp Ala Val Met Val Lys Asp Val Asn Glu Asp Leu Met
35 40 45
Lys Gly Tyr Asp Ile Phe Thr Pro Ile Ala Ala Thr Asp Leu Gly Phe
50 55 60
Glu Pro Gly Ile Pro Val Ile Glu Ala Gly Pro Ile Leu Phe Arg Ile
65 70 75 80
Pro Ala Met Ser Ala Pro Val Phe Asp Asn Ile Arg Leu Pro Ala Lys
85 90 95
Gln Asn Met Val
100

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

Met Asn Thr Lys Met Met Ser Gln Phe Ser Val Met Asp Asn Glu Met
1 5 10 15
Leu Ala Cys Val Glu Gly Gly Asp Ile Asp Trp Gly Arg Glu Ile Ser
20 25 30
Cys Ala Ala Gly Val Ala Tyr Gly Ala Ile Asp Gly Cys Ala Thr Thr
35 40 45
Val

(2) INFORMATION FOR SEQ ID NO:233:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

Met Arg Glu Lys Glu Ile Phe Asp Ser Ile Val Thr Ile Ile Gln Glu
1 5 10 15
Arg Gln Gly Glu Asp Phe Val Val Thr Glu Ser Leu Ser Leu Lys Asp
20 25 30
Asp Leu Asp Ala Asp Ser Val Asp Leu Met Glu Phe Ile Leu Thr Leu
35 40 45
Glu Asp Glu Phe Ser Ile Glu Ile Ser Asp Glu Glu Ile Asp Gln Leu
50 55 60
Gln Ser Val Gly Asp Val Val Lys Ile Ile Gln Gly Lys
65 70 75

(2) INFORMATION FOR SEQ ID NO:234:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

Met Ala His Gly Asp Leu Leu Tyr His Asp Gly Leu Phe Phe Ser Ala
1 5 10 15
Lys Lys Glu Asp Gly Thr Tyr Asp Phe His Glu Asn Phe Glu Tyr Val
20 25 30
Thr Pro Trp Leu Lys Gln Val Asp
35 40

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

Met Ser Leu Ile Thr His Arg Arg Phe Ile Ser Cys Asn Glu Asn Ile
1 5 10 15
Lys His Tyr Lys Arg Leu Ile Asp Lys Ala Glu Lys Cys Val Asn Asp
20 25 30
Leu Met Ala Glu Leu Asn Ser Val Ile Thr Thr Val Thr Gly Ile Glu
35 40 45
Asn Arg Leu Gly Ala Val Ile Leu Ala Glu Ile Arg Asn Ile His Ala
50 55 60
Phe Asp Asn Pro Ala Gln Leu Gln Ala Phe Ala Gly Leu Asp Ser Ser
65 70 75 80
Ile Tyr Gln Ser Gly Gln Ile Asp Leu Val Gly Arg Met Val Lys Arg
85 90 95
Gly Ser Leu His Leu Arg
100

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

Met	Ile	Arg	Ala	Val	Phe	Phe	Ser	Ile	Asp	Asn	Asp	Met	Glu	Glu	Ala		
1					5				10				15				
Ala	Arg	Ser	Met	Gly	Ala	Ser	Ser	Phe	Tyr	Thr	Met	Val	Arg	Val	Ile		
			20						25				30				
Ile	Pro	Tyr	Ile	Leu	Pro	Val	Val	Leu	Ser	Val	Val	Val	Leu	Asn	Phe		
	35					40							45				
Asn	Ser	Leu	Leu	Ser	Asp	Tyr	Asp	Leu	Ser	Val	Phe	Leu	Tyr	His	Pro		
	50						55					60					
Leu	Phe	Gln	Pro	Leu	Gly	Ile	Val	Ile	Lys	Gln	Ser	Thr	Asp	Glu	Thr		
	65					70			75				80				
Ala	Thr	Leu	Asn	Ala	Gln	Ala	Met	Met	Phe	Val	Tyr	Ser	Val	Ile	Leu		
		85							90				95				
Met	Ile	Met	Ser	Ser	Ala	Ala	Leu	Tyr	Leu	Ser	Ser	Leu	Phe	Gln	Gly		
			100						105				110				
Lys	Arg	Gly	Lys	Arg													
		115															

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

Met	Glu	Lys	Cys	Tyr	Thr	Asp	Val	Thr	Glu	Phe	Ala	Ile	Pro	Ala	Ser	
1					5				10				15			
Thr	Gln	Lys	Leu	Tyr	Leu	Ser	Pro	Val	Leu	Asp	Gly	Phe	Asn	Ser	Glu	
			20					25					30			

Ile Ile Ala Tyr Asn Leu Ser Thr Ser Pro Asn Leu Glu Gln Val Gln
 35 40 45
 Thr Met Leu Glu Gln Ala Phe Thr Glu Lys His Tyr Glu Asn Thr Ile
 50 55 60
 Leu His Ser Asp Gln Gly Trp Gln Tyr Gln His Asp Ser Tyr His Arg
 65 70 75 80
 Phe Leu Arg Val Arg Glu Phe Lys His Leu Cys His Ala Arg Glu Thr
 85 90 95
 Ala Lys Thr Thr Val
 100

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

Met Glu Ile Leu Thr Thr Gln Gln Val Arg Glu Gly Tyr Gln Ala Ile
 1 5 10 15
 Leu Ala Ser Pro Leu Gly Leu Gln Asp Ala Phe Glu Val Ala Gln Glu
 20 25 30
 Lys Ser Gly Ser Tyr Thr Val Pro Pro Glu Ile Asp Gly Trp Lys Gly
 35 40 45
 Asn Thr Glu Pro Leu Arg Ile Asp Tyr Val Phe Thr Thr Lys Glu Leu
 50 55 60
 Ala Val Glu Asn Leu His Val Val Phe Asp Gly Asn Lys Ser Pro Gln
 65 70 75 80
 Val Ser Asp His Tyr Gly Leu Asn Ala Met Leu Asn Trp Lys
 85 90

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

Met Leu Lys His Leu Asn Leu Lys Gly His Leu Leu Thr Ala Ile Ser
1 5 10 15
Tyr Met Ile Pro Ile Val Cys Gly Ala Gly Phe Leu Val Ala Ile Gly
20 25 30
Leu Ala Met Gly Gly Val Pro Asp Ala Leu Val Ala Gly Lys Phe
35 40 45
Thr Ile Trp Asp Ala Leu Ala Thr Met Gly Gly Lys Ala Leu Gly Leu
50 55 60
Leu Pro Val Val Ile Ala Thr Gly Leu Ser Tyr Ser Ile Ala Gly Lys
65 70 75 80
Pro Gly Ile Ala Pro Gly Phe Val Val Gly Leu Ile Ala Asn Ser Val
85 90 95
Gly Ser Gly Phe Ile Gly Gly Ile Leu Gly Gly Tyr Ile Val Gly Phe
100 105 110
Leu Val Gln Ala Ile Ile Lys Lys Val Lys Val Pro Asn Trp Ile Lys
115 120 125
Gly Leu Met Pro Thr Leu Ile Ile Pro Phe Val Pro Leu Trp
130 135 140

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

Met Ile Ala Leu Gly Trp Ser Asn Ile Gly Ala Ala Ile Ala Pro Asp
1 5 10 15
Ala Ala Leu Ala Ser Val Ala Ala Ala Ile Ile Met Val Leu Gly Gly
20 25 30
Asp Phe Thr Lys Thr Gly Ile Gly Val Ala Gln Ala Val Ala Ile Pro
35 40 45
Leu Ala Val Ala Gly Leu Phe Leu Thr Met Ile Val Arg Thr Ile Ser
50 55 60

Val Gly Leu Val His Thr Ala Asp Ala Ala Lys Lys Gly Asp Phe
 65 70 75 80
 Gly Ala Val Glu Arg Ala His Phe Ile Ala Leu Leu Phe Gln Gly Leu
 85 90 95
 Arg Ile Ala Leu Pro Ala Ala Leu Leu Met Val Pro Thr Glu Thr
 100 105 110
 Val Gln Ser Ile Leu Ser Ala Met Pro Asp Trp Leu Lys Asp Gly Met
 115 120 125
 Ala Ile Gly Gly Met Val Val Ala Val Gly Tyr Ala Met Val Ile
 130 135 140
 Asn Met Met Ala Thr Arg Glu Val Trp Pro Phe Phe Ala Leu Gly Phe
 145 150 155 160
 Val Leu Ala Ala Val Ser Asp Ile Thr Leu Ile Gly Phe Gly Ala Ile
 165 170 175
 Gly Val Ala Ile Ala Leu Ile Tyr Leu His Leu Ser Lys Thr Gly Gly
 180 185 190
 Asn Gly Gly Gly Ala Ala Thr Ser Asn Asp Pro Ile Gly Asp Ile
 195 200 205
 Leu Glu Asp Tyr
 210

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

Met Leu Asp Val Glu Ala Ile Arg Lys Asp Phe Pro Ile Leu Asp Gln
 1 5 10 15
 Ile Val Asn Asp Glu Pro Leu Val Tyr Leu Asp Asn Ala Ala Thr Thr
 20 25 30
 Gln Lys Pro Leu Val Val Leu Lys Ala Ile Asn Ser Tyr Tyr Glu Gln
 35 40 45
 Asp Asn Ala Asn Val His Arg Gly Val His Thr Leu Ala Glu Arg Ala
 50 55 60
 Thr Ala Ser Leu
 65

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

Met Thr Lys Leu Leu Asn Lys Lys Trp Lys Val Lys Ile Met Lys Gln
1 5 10 15
Ile Leu Leu Val Cys Asn Ala Gly Met Ser Thr Ser Met Leu Val Lys
20 25 30
Lys Met Gln Gln Ser Ala Thr Glu Arg Gly Ile Glu Ile Ser Ile Gln
35 40 45
Ala Lys Ser Met Thr Glu Ala Lys Lys Asn Ile His Glu Ala Asp Val
50 55 60
Ile Leu Ile Gly Pro Gln Ile Arg Tyr Glu Leu Leu Ala Val Lys Glu
65 70 75 80
Ile Ala Gly Asn Ile Pro Val Asp Thr Ile Asp Met Arg Asp Tyr Gly
85 90 95
Met Met Asn Gly Ala Lys Val Leu Glu Gln Ala Leu Glu Trp Ile Gly
100 105 110
Glu Ile Arg
115

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

Met Val Leu Met Gln Lys Met His Gly Lys Glu Leu Ile Thr Leu Asn
1 5 10 15

Gln Thr Val Lys Trp Tyr Lys Val Ser Gly Phe Met Ile Leu Leu Thr
20 25 30
Lys Pro Trp Tyr Tyr Leu Lys Ser Asp Gly Ser Tyr Ala Arg Asn Ala
35 40 45
Trp Gln Gly Asn Tyr Tyr Leu Lys Ser Asp Gly Lys Met Ala Val Asn
50 55 60
Glu Trp Val Tyr Asp Ala Thr Tyr Gln Ala Trp Tyr Tyr Leu Thr Ser
65 70 75 80
Asp Gly Ser Tyr Ala Tyr Ser Thr Trp Gln Gly Asn Tyr Tyr Pro Lys
85 90 95
Ile Gly Trp

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

Met Leu Thr Val His Gly Lys Glu Ile Thr Ile Leu Lys Ser Asp Gly
1 5 10 15
Lys Met Ala Val Asn Glu Trp Val Asp Gly Gly Arg Tyr Tyr Val Gly
20 25 30
Ala Asp Gly Val Trp Lys Glu Gly Gln Ala Ser Thr Ala Ser Pro Ser
35 40 45
Asn Asp Ser Asn Ser Glu Tyr Ser Cys Cys Phe Arg Lys Gly Lys Lys
50 55 60
Leu
65

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

Met Asn Asn Asn Phe Asn Asn Phe Asn Asn Met Asp Asp Leu Phe Asn
1 5 10 15
Gln Leu Met Gly Gly Met Arg Gly Tyr Ser Ser Glu Asn Arg Arg Tyr
20 25 30
Leu Ile Asn Gly Arg Glu Val Thr Pro Glu Glu Phe Ala His Tyr Arg
35 40 45
Thr Thr Gly Gln Leu Pro Gly Asn Ala Glu Thr Asp Val Gln Met Pro
50 55 60
Gln Gln Ala Ser Gly Met Lys Gln Asp Gly Val Leu Ala Lys Leu Gly
65 70 75 80
Arg Asn Leu Thr Ala Glu Ala Arg Glu Gly Lys Leu Asp Pro Val Ile
85 90 95
Gly Arg Asn Lys Glu Ile Gln Glu Thr Ser Glu Ile Leu Ser Arg Arg
100 105 110
Thr Lys Asn Asn Pro Val Leu Val Gly Asp Ala Gly Val Gly Lys Thr
115 120 125
Ala Val Val Glu Gly Leu Ala Gln Ala Ile Val Asn Gly Asp Val Pro
130 135 140
Ala Ala Ile Lys Asn Lys Glu Ile Ile Ser Ile Asp Ile Ser Gly Leu
145 150 155 160
Glu Ala Gly Thr Gln Tyr Arg Gly Ser Phe Glu Glu Asn Val Gln Asn
165 170 175
Leu Val Asn Glu Val Lys Glu Ala Gly Asn Ile Ile Leu Phe Phe Asp
180 185 190
Glu Ile His Gln Ile Leu Gly Ala Gly Ser Thr Cys Gly Asp Ser Gly
195 200 205
Ser Lys Gly Leu Ala Asp Ile Leu Ser Gln Ser Ile Ser Leu Val Glu
210 215 220
Asn
225

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

Met Thr Ile Phe Pro Asp Asp Phe Leu Trp Gly Gly Ala Val Ala Ala
1 5 10 15
Asn Gin Val Glu Gly Ala Tyr Asn Glu Asp Gly Lys Gly Leu Ser Val
20 25 30
Gln Asp Val Leu Pro Lys Gly Gly Leu Gly Glu Ala Thr Glu Asn Pro
35 40 45
Thr Glu Asp Asn Leu Lys Leu Ile Gly Ile Asp Phe Tyr His Lys Tyr
50 55 60
Lys Glu Asp Ile Ser Leu Phe Ser Glu Met Gly Phe Asn Val Phe Arg
65 70 75 80
Thr Ser Ile Ala Trp Ser Arg Ile Phe Pro Lys Gly Asp Glu Glu Glu
85 90 95
Pro Asn Glu Ala Gly Leu Lys Tyr Tyr Asp Glu Leu Phe Asp Glu Leu
100 105 110
His Ala His Gly Ile Glu Pro Leu Val Thr Leu Ser His Tyr Glu Thr
115 120 125
Pro Leu Tyr Leu Ala Arg Lys Tyr His Gly Trp Ile Asp Arg Lys Asn
130 135 140
Asp Ser Phe Leu
145

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

Met Ile Glu Tyr Lys Asn Val Ala Leu Arg Tyr Thr Glu Lys Asp Val
1 5 10 15
Leu Arg Asp Val Asn Leu Gln Ile Glu Asp Gly Glu Phe Met Val Leu
20 25 30
Val Gly Pro Ser Gly Ser Gly Lys Thr Thr Met Leu Lys Met Ile Asn
35 40 45
Arg Leu Leu Glu Pro Thr Asp Gly Asn Ile Tyr Met Asp Gly Lys Arg
50 55 60

Ile Lys Asp Tyr Asp Glu Arg Glu Leu Arg Leu Ser Thr Gly Tyr Val
65 70 75 80
Leu Gln Ala Ile Ala Leu Phe Pro Asn Leu Thr Val Ala Glu Asn Ile
85 90 95
Ala Leu Ile Pro Glu Met Lys Gly Trp Ser Lys Glu Glu Ile Thr Lys
100 105 110
Lys Thr Glu Glu Leu Leu Ala Lys Val Gly Leu Pro Val Ala Glu Tyr
115 120 125
Gly His Arg Leu Pro Ser Glu Leu Ser Gly Gly Glu Gln Gln Arg Val
130 135 140
Gly Ile Val Arg Ala Met Ile Gly Gln Pro Lys Ile Phe Leu Met Asp
145 150 155 160
Glu Pro Phe Ser Ala Leu Asp Ala Ile Ser Arg Lys Gln Leu Gln Val
165 170 175
Leu Thr Lys Glu Leu His Lys Glu Phe Gly Met Thr Thr Ile Phe Val
180 185 190
Thr His Asp Thr Asp Glu Ala Leu Lys Leu Ala Asp Arg Ile Ala Val
195 200 205
Leu Gln Asp Gly Glu Ile Arg Gln Val Ala Asn Pro Glu Thr Ile Leu
210 215 220
Lys Val Pro Ala Thr Asp Phe Val Ala Asp Leu Phe Gly Gly Ser Val
225 230 235 240
His Asp

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

Met Pro Phe Val Pro Gly Ile Ala Leu Thr Asn Ala Val Arg Asp Ile
1 5 10 15
Met Thr Asn His Ile Asn Ser Gly Met Ser Lys Met Phe Glu Ser Leu
20 25 30
Leu Ile Thr Leu Ala Leu Gly Ala Gly Thr Ser Val Ala Leu Val Leu
35 40 45

Met Asn

50

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

Met	Tyr	Thr	Ile	Arg	Met	Leu	Lys	Met	Gly	Ser	Glu	Ala	Ala	Ala	Lys
1					5						10				15
Ser	Ala	Gln	Glu	His	Gly	Leu	Lys	Ser	Val	Glu	Val	Thr	Val	Lys	Gly
						20				25				30	
Pro	Gly	Ser	Gly	Arg	Glu	Ser	Ala	Ile	Ser	Cys	Ala	Cys	Cys	Arg	Trp
							35			40				45	
Ser															

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

Met	Ile	Glu	Phe	Glu	Lys	Pro	Asn	Ile	Thr	Lys	Ile	Asp	Glu	Asn	Lys
1						5					10				15
Asp	Tyr	Gly	Lys	Leu	Val	Ile	Glu	Pro	Leu	Glu	Arg	Gly	Tyr	Gly	Thr
						20				25				30	
Ala	Leu	Gly	Asn	Ser	Leu	Arg	Arg	Val	Leu	Leu	Ala	Ser	Leu	Pro	Gly
						35				40				45	
Ala	Ala	Val	Thr	Ser	Ile	Asn	Ile	Asp	Gly	Val	Leu	His	Glu	Phe	Asp
							50			55				60	

Thr Val Pro Gly Val Arg Glu Asp Val Met Gln Ile Ile Leu Asn Ile
65 70 75 80
Lys Gly Ile Ala Val Lys Ser Tyr Val Glu Asp Glu Lys Ile Ile Glu
85 90 95
Leu Asp Val Glu Gly Pro Ala Glu Val Thr Ala Gly Asp Ile Leu Thr
100 105 110
Asp Ser Asp Ile Glu Ile Val Asn Pro Asp His Tyr Leu Phe Thr Ile
115 120 125
Gly Glu Gly Ser Ser Leu Lys Ala Thr Met Thr Val Asn Ser Gly Arg
130 135 140
Gly Tyr Val Pro Ala Asp Glu Asn Lys Lys Asp Asn Ala Pro Val Gly
145 150 155 160
Thr Leu Ala Val Asp Ser Ile Tyr Thr Pro Val Thr Lys Val Asn Tyr
165 170 175
Gln Val Glu Pro Ala Arg Val Gly Ser Asn Asp Gly Phe Asp Lys Leu
180 185 190
Thr Leu Glu Ile Leu Thr Asn Gly Thr Ile Ile Pro Glu Asp Ala Leu
195 200 205
Gly Leu Ser Ala Arg Ile Leu Thr Glu His Leu Asp Leu Phe Thr Asn
210 215 220
Leu Thr Glu Ile Ala Lys Ser Thr Glu Val Met Lys Glu Ala Asp Thr
225 230 235 240
Glu Ser Asp Asp Arg Ile Leu Asp Arg Thr Ile Glu Glu Leu Asp Leu
245 250 255
Ser Val Arg Ser Tyr Asn Cys Leu Lys Arg Ala Gly Ile Asn Thr Val
260 265 270
His Asp Leu Thr Glu Lys Ser Glu Ala Glu Met Met Lys Val Arg Asn
275 280 285
Leu Gly Arg Lys Ser Leu Glu Glu Val Lys Leu Lys Leu Ile Asp Leu
290 295 300
Gly Leu Gly Leu Lys Asp Lys
305 310

(2) INFORMATION FOR SEQ ID NO:251:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 151 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

Met Asp Ile Glu Lys Gln Arg Gly Ile Ser Val Thr Ser Ser Val Met
 1 5 10 15
 Gln Phe Asp Tyr Asp Gly Lys Arg Val Asn Ile Leu Asp Thr Pro Gly
 20 25 30
 His Glu Asp Phe Ser Glu Asp Thr Tyr Arg Thr Leu Met Ala Val Asp
 35 40 45
 Ala Ala Val Met Val Val Asp Ser Ala Lys Gly Ile Glu Ala Gln Thr
 50 55 60
 Lys Lys Leu Phe Glu Val Val Lys His Arg Gly Ile Pro Val Phe Thr
 65 70 75 80
 Phe Met Asn Lys Leu Asp Arg Asp Gly Arg Glu Pro Leu Asp Leu Leu
 85 90 95
 Gln Glu Leu Glu Glu Ile Leu Gly Ile Ala Ser Tyr Pro Met Asn Trp
 100 105 110
 Pro Ile Gly Met Gly Lys Ala Phe Glu Gly Leu Tyr Asp Leu Tyr Asn
 115 120 125
 Gln Arg Leu Glu Leu Tyr Lys Gly Asp Glu Arg Phe Ala Ser Pro Arg
 130 135 140
 Arg Trp Arg Gln Thr Phe Trp
 145 150

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

Met Ala Val Ile Ala Glu Arg Lys Ala Tyr Tyr His Asp Pro Val Glu
 1 5 10 15
 Asp Ala Ile Ile Met Lys Arg Glu Ile Asp Glu Gly
 20 25

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

Met Asn Glu Thr Trp Ser Arg Thr Ala Leu Thr Leu Leu Lys His Gly
1 5 10 15
Ser Glu Val Asn Leu Glu Arg Ala Leu Ser Val Asn Gly Arg Leu Gly
20 25 30
Gly His Val Val Thr Gly His Ile Asp Gly Thr Gly Lys Ile Ser Ser
35 40 45
Ile Lys Lys Asp Asp Asn Ala Val Trp Tyr Gln Ile Asn Thr Gln Lys
50 55 60
Glu Ile Leu Asp Leu Ile Val Glu Lys Gly Ser Ile Thr Ile Asp Gly
65 70 75 80
Ile Ser Leu Thr Val Ala Lys Val Ser Lys Val Asn Phe Ser Val Ser
85 90 95
Val Ile Pro His Thr Leu Lys Gln Thr Ile Leu Lys Ser Lys Gln Val
100 105 110
Gly Ser Thr Val Asn Leu Glu Asn Asp Ile Leu Gly Lys Tyr Val Gln
115 120 125
Lys Leu Met Asp Asn Ser Pro Lys Ser Glu Ile Ser Lys Glu Leu Leu
130 135 140
Tyr Gln Asn Gly Phe
145

(2) INFORMATION FOR SEQ ID NO:254:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 70 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

Met Asn Trp Ser Ala Leu Glu Gln Gln Ile Val Asp Glu Leu Lys Ile
1 5 10 15
Tyr Ile Ala Pro Lys Ile Phe Gly Gly Ser Ala Lys Phe Pro Val Gly
20 25 30

Gly Glu Gly Ile Ser Leu Pro Asn Asp Ala Ile Arg Leu Lys Pro Tyr
 35 40 45
 Ala Phe Ser Gln Xaa Gly Xaa Asp Tyr Leu Ile Glu Ser Glu Val Ile
 50 55 60
 Tyr Pro Cys Ser Gln Glu
 65 70

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

Met Val Leu Phe Leu Val Pro Gln Leu Arg Asn Ala Tyr Gly Thr Ala
 1 5 10 15
 Ala Ile Gly Ile Ile Cys Gly Leu Tyr Trp Ala Val Ser Ser Asn Met
 20 25 30
 Thr Val Glu Ala Thr Gln Arg Leu Thr Gly Gly Gly Phe Ala Ile
 35 40 45
 Gly His Gln Gln Gln Phe Ala Ile Trp Phe Val Asp Lys Val Ala Gly
 50 55 60
 Arg Phe Gly Lys Lys Glu Glu Ser Leu Asp Asn Leu Lys Leu Pro Lys
 65 70 75 80
 Phe Leu Ser Ile Phe His Asp Thr Val Val Ala Ser Ala Thr Phe Asp
 85 90 95
 Ala Arg Ile Leu Arg Gly His Ser Phe Asn Leu Gly Ser Arg His Tyr
 100 105 110
 Val

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

Met Leu Ile Asn Ser Leu Asn Gln Ser Tyr Ile Ser Ala Lys Arg Ile
1 5 10 15
Glu Glu Val Phe Ala Glu Ser Pro Glu Asn Ile His Ser Glu Leu Glu
20 25 30
Gln Lys Gln Val Thr Ser Gly Arg Val Leu Gln Val Gln Glu Leu Thr
35 40 45
Phe Thr Tyr Pro Asp Ala Ala Gln Pro Ser Leu Arg Asp Ile Ser Phe
50 55 60
Asp Met Thr Gln Gly Gln Ile Leu Gly Ile Ile Gly Gly Thr Gly Ser
65 70 75 80
Gly Lys Ser Ser Leu Val Gln Leu Leu Gly Leu Tyr Pro Val Asp
85 90 95
Lys Gly Asn Ile Asp Leu Tyr Gln Asn Gly Arg Ser Pro Leu Asn Leu
100 105 110
Glu Gln Trp Arg Ser Trp Ile Ala Tyr Val Pro Gln Lys Val Lys Leu
115 120 125
Phe Lys Gly Thr Ile Arg Ser Asn Leu Thr Leu Gly Leu Asn Gln Glu
130 135 140
Val Ser Asp Gln Lys Leu Trp Gln Ala Leu Glu Ile Ala Gln Ala Lys
145 150 155 160
Asp Phe Val Ser Glu Lys Glu Gly Leu Leu Asp Ala Leu Ile Glu Ala
165 170 175
Gly Gly Arg Asn Phe Ser Gly Gly Gln Lys Gln Arg Leu Ser Ile Ala
180 185 190
Arg Ala Val Leu Arg Gln Ala Pro Phe Ile Ile Leu Asp Asp Ala Thr
195 200 205
Ser Ala Leu Asp Thr Ile Thr Glu Ser Lys Leu Leu Lys Ala Ile Arg
210 215 220
Glu Asn Phe Pro Asn Thr Ser Leu Ile Leu Ile Ser Gln Arg Thr Ser
225 230 235 240
Thr Leu Gln Met Ala Asp Gln Ile Leu Leu Glu Lys Gly Glu Leu
245 250 255
Leu Ala Val Gly Lys His Asp Asp Leu Met Lys Ser Ser Gln Val Tyr
260 265 270
Arg Glu Ile Asn Ala Ser Gln His Gly Lys Glu Asp
275 280

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

Met Lys Asp Pro Glu Ser Arg Leu Tyr Ile Leu Leu Lys Asp Gly Gln
1 5 10 15
Val Ile Gly Thr Cys Thr Val Asp Leu Ser Thr Asn Thr Asn Tyr Phe
20 25 30
Tyr Gly Leu Ala Ile Leu Glu Pro Glu Arg Gly Lys Gly Tyr Gly Ser
35 40 45
Tyr Leu Ala Lys Ser Leu Val Asn Gln Leu Ile Glu Gln Asn Asp Lys
50 55 60
Glu Phe Gln Ile Ala Val Glu Asp Ser Asn Val Gly Ala Lys Arg Leu
65 70 75 80
Tyr Glu Lys Ile Gly Phe Val Lys Gln Thr Gln Val Val Tyr Leu Asn
85 90 95
Glu Lys Gly Ala Arg Asp Ser Glu Val
100 105

(2) INFORMATION FOR SEQ ID NO:258:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 213 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

Met Phe Ala Leu Ser Ser Asn Lys Glu Leu Ala Glu Arg Val Ala Gln
1 5 10 15
Glu Ile Gly Ile Glu Leu Gly Lys Ser Ser Val Arg Gln Phe Ser Asp
20 25 30
Gly Glu Ile Gln Val Asn Ile Glu Glu Ser Ile Arg Gly Lys His Val
35 40 45
Phe Ile Leu Gln Ser Thr Ser Ser Pro Val Asn Asp Asn Leu Leu Glu
50 55 60

Ile	Leu	Ile	Met	Val	Asp	Ala	Leu	Lys	Arg	Ala	Ser	Ala	Glu	Ser	Val
65				70				75							80
Asn	Val	Val	Met	Pro	Tyr	Tyr	Gly	Tyr	Ala	Arg	Gln	Asp	Arg	Lys	Ala
					85				90						95
Arg	Ala	Arg	Glu	Pro	Ile	Thr	Ser	Lys	Leu	Val	Ala	Asn	Met	Leu	Glu
					100				105						110
Val	Ala	Gly	Val	Asp	Arg	Leu	Leu	Thr	Ile	Asp	Leu	His	Ala	Ala	Gln
					115				120						125
Ile	Gln	Gly	Phe	Phe	Asp	Ile	Pro	Val	Asp	His	Leu	Met	Gly	Ala	Pro
					130				135						140
Leu	Ile	Ala	Asp	Tyr	Phe	Glu	Arg	Pro	Gly	Met	Val	Gly	Ser	Asp	Tyr
					145				150			155			160
Val	Val	Val	Ser	Pro	Asp	His	Gly	Gly	Val	Thr	Arg	Ala	Arg	Lys	Leu
					165				170						175
Ala	Glu	Phe	Leu	Lys	Thr	Ser	Ile	Ala	Ile	Ile	Glu	Lys	Arg	Arg	Ser
					180				185						190
Val	Asp	Lys	Met	Asn	Thr	Ser	Glu	Val	Met	Asn	Thr	Ile	Gly	Lys	Val
					195				200						205
Glu	Gly	Asn	His	Leu											
					210										

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

Met	Ile	Ser	Phe	Leu	Leu	Leu	Leu	Val	Leu	Val	Trp	Gly	Phe	Tyr	Ile
1				5					10						15
Gly	Tyr	Arg	Arg	Gly	Leu	Leu	Leu	Gln	Val	Tyr	Tyr	Leu	Ile	Ser	Ala
					20				25						30
Met	Ala	Ser	Ala	Phe	Met	Ala	Gly	Gln	Phe	Tyr	Lys	Gly	Leu	Gly	Glu
					35				40						45
Gln	Phe	His	Leu	Leu	Leu	Pro	Tyr	Ala	Asn	Ser	Gln	Glu	Gly	Gln	Gly
					50				55						60
Thr	Phe	Phe	Phe	Pro	Ser	Asp	Gln	Leu	Phe	Gln	Leu	Asp	Lys	Val	Phe
					65				70						80

Tyr	Ala	Gly	Ile	Gly	Tyr	Leu	Leu	Val	Phe	Gly	Ile	Val	Tyr	Ser	Ile
					85					90					95
Gly	Arg	Leu	Leu	Gly	Leu	Leu	Leu	His	Leu	Ile	Pro	Ser	Lys	Lys	Leu
					100				105					110	
Gly	Gly	Lys	Leu	Phe	Gln	Val	Ser	Ala	Gly	Ile	Leu	Ser	Met	Leu	Val
					115				120					125	
Thr	Leu	Phe	Val	Leu	Gln	Met	Ala	Leu	Thr	Ile	Leu	Ala	Thr	Ile	Pro
					130				135					140	
Met	Ala	Val	Ile	Gln	Asn	Pro	Leu	Glu	Lys	Ser	Ile	Val	Ala	Lys	His
					145				150			155		160	
Ile	Ile	Gln	Ser	Ile	Pro	Ile	Thr	Thr	Ser	Trp	Leu	Lys	Gln	Ile	Trp
					165				170					175	
Val	Thr	Asn	Leu	Ile	Gly										
					180										

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

Met	Arg	Ala	Phe	Ser	Asp	Phe	Gly	Thr	Pro	Met	Leu	Ile	Gly	Glu	Gly
1						5				10					15
Tyr	Arg	Thr	Phe	Pro	Val	Leu	Ile	Tyr	Thr	Gln	Phe	Ile	Ser	Glu	Val
						20				25					30
Gly	Gly	Asn	Ser	Ala	Phe	Ala	Ile	Met	Ala	Ile	Ile	Ile	Ala	Leu	Ala
						35				40					45
Ile	Phe	Leu	Ile	Gln	Lys	His	Ile	Ala	Asn	Arg	Tyr	Ser	Phe	Ser	Met
						50				55					60
Asn	Leu	Leu	His	Pro	Ile	Glu	Pro	Lys	Lys	Thr	Thr	Lys	Gly	Lys	Met
						65				70			75		80
Ala	Ala	Ile	Tyr	Ala	Thr	Val	Tyr	Gly	Ile	Ile	Phe	Ile	Ser	Val	Leu
						85				90					95
Pro	Gln	Ile	Tyr	Leu	Ile	Tyr	Thr	Ser	Phe	Leu	Lys	Thr	Ser	Gly	Met
						100				105					110
Val	Phe	Val	Lys	Gly	Tyr	Ser	Pro	Asn	Ser	Tyr	Lys	Val	Ala	Phe	Asn
						115				120					125

Arg Met Gly Ser Ala Ile Phe Asn Thr Ile Arg Ile Pro Leu Ile Ala		
130	135	140
Leu Val Leu Val Val Pro Ile Tyr Asp Ile Tyr Leu Leu Pro Ser Arg		
145	150	155
		160

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

Met Val Pro Tyr Ile Val Pro Gly Thr Val Leu Gly Ile Ala Phe Ile			
1	5	10	15
Ser Ser Phe Asn Thr Gly Leu Phe Gly Ser Gly Phe Leu Met Ile Thr			
20	25	30	
Gly Thr Ala Phe Ile Leu Ile Met Ser Leu Ser Val Arg Arg Leu Pro			
35	40	45	
Tyr Thr Ile Arg Ser Ser Val Ala Ser Leu Gln Gln Ile Ala Pro Ser			
50	55	60	
Ile Glu Glu Ala Ala Gly Lys Leu Arg Lys			
65	70		

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

Met Ile Phe Ile Pro Met Ala Ala Tyr Ser Ile Ala Arg Asn Met Ser			
1	5	10	15
Lys Arg Lys Ala Phe Thr Ile His Val Tyr Pro Leu Asn Pro Arg Asn			
20	25	30	

Leu Arg Thr Phe Pro Ser His His Asp Ser Asp Tyr Gly Tyr Asp Glu
35 40 45

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

Met Lys Phe Arg Lys Leu Ala Cys Thr Val Leu Ala Gly Ala Ala Val
1 5 10 15
Leu Gly Leu Ala Ala Cys Gly Asn Ser Gly Gly Ser Lys Asp Ala Ala
20 25 30
Lys Ser Gly Gly Asp Gly Ala Lys Thr Glu Ile Thr Trp Trp Ala Phe
35 40 45
Pro Val Phe Thr Gln Glu Lys Thr Gly Asp Gly Val Gly Thr Tyr Glu
50 55 60
Lys Ser Ile Ile Gln Ala Phe
65 70

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

Met Asn Ser Gln Gln Lys Pro Gln Glu Ile Lys Val Glu Glu Pro Val
1 5 10 15
Glu Ser Lys Glu Glu Thr Val Asn Gln Pro Val Glu Gln Pro Lys Val
20 25 30
Glu Thr Pro Ala Val Glu Lys Gln Thr Glu Pro Thr Glu Glu Pro Lys
35 40 45

Val Glu Val Thr Ser Ile Pro Gln Thr Thr Arg Tyr Glu Glu Asp Leu
50 55 60
Thr Lys Glu His Gly Thr Arg Glu Val Val Lys Glu Gly Lys Asn Gly
65 70 75 80
Ser Arg Thr Val Thr Thr Pro Tyr Ile Leu Asn Ala Thr Asp Gly Thr
85 90 95
Thr Thr Glu Gly Thr Ser Thr Asp Glu Ala Glu Met Glu Lys Glu
100 105 110
Val Val Arg Val Gly Thr Lys Pro Lys Glu Lys Leu Ala Pro Val Leu
115 120 125
Ser Leu Thr Ser Val Thr Asp Asn Ala Met Leu Arg Ser Ala Arg Leu
130 135 140
Thr Tyr His Leu Glu Asn Thr Asp Ser Val Asp Val Lys Lys Ile His
145 150 155 160
Ala Glu Ile Lys Asn Gly Asp Lys Val Val Lys Thr Ile Asp Leu Ser
165 170 175
Lys Glu Arg Leu Ser Asp Ala Val Asp Gly Leu Glu Leu Tyr Lys Asp
180 185 190
Tyr Lys Ile Val Thr Ser Met Thr Tyr Asp Arg Gly Asn Gly Glu Glu
195 200 205
Thr Ser Thr Leu Glu Glu Thr Pro Leu Arg Leu Asp Leu Lys Lys Val
210 215 220
Glu Leu Lys Asn Ile Gly Ser Thr Asn Leu Val Lys Val Asn Glu Asp
225 230 235 240
Gly Thr Glu Val Ala Ser Asp Phe Leu Thr Ser Lys Pro Val Asp Val
245 250 255
Gln Asn Tyr Tyr Leu Lys Val Thr Ser Arg Asp Asn Lys Val Val Ser
260 265 270
Pro Pro Ser
275

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

Met Ala Val Met Lys Ile Glu Tyr Tyr Ser Gln Val Leu Asp Met Glu
 1 5 10 15
 Trp Gly Val Asn Val Leu Tyr Pro Asp Ala Asn Arg Val Glu Glu Pro
 20 25 30
 Glu Cys Glu Asp Ile Pro Val Leu Tyr Leu Leu His Gly Met Ser Gly
 35 40 45
 Asn His Asn Ser Trp Leu Lys Arg Thr Asn Val Glu Arg Leu Leu Arg
 50 55 60
 Gly Thr Asn Leu Ile Val Val Met Pro Asn Thr Ser Asn Gly Trp Tyr
 65 70 75 80
 Thr Asp Thr Gln Tyr Gly Phe Asp Tyr Tyr Thr Ala Leu Ala Glu Glu
 85 90 95
 Leu Pro Gln Val Pro Glu Thr Leu Leu Pro
 100 105

(2) INFORMATION FOR SEQ ID NO:266:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

Met Arg Leu Leu Ala Met Lys Met Lys Gln Ile Ser Asp Thr Thr Leu
 1 5 10 15
 Lys Ile Thr Met Ser Leu Glu Asp Leu Met Asp Arg Gly Met Glu Ile
 20 25 30
 Ala Asp Phe Leu Val Pro Gln Glu Lys Thr Glu Glu Phe Phe Tyr Ala
 35 40 45
 Ile Leu Gly
 50

(2) INFORMATION FOR SEQ ID NO:267:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

Met Leu Pro Ile Ile Cys Cys Gly Glu Ser Leu Glu Thr Tyr Glu Ala
1 5 10 15
Gly Lys Ala Ala Glu Phe Val Gly Ala Gln Val Ser Ala Ala Leu Ala
20 25 30
Gly Leu Thr Ala Glu Gln Val Ala Ala Ser Val Ile Ala Tyr Glu Pro
35 40 45
Ile Trp Ala Ile Gly Thr Gly Lys Ser Ala Ser Gln Asp Asp Ala Gln
50 55 60
Lys Met Cys Lys Val Val Arg Asp Val Val Ala Ala Asp Phe Gly Gln
65 70 75 80
Glu Val Ala Asp Lys Val Arg Val Gln Tyr Gly Gly Ser Val Lys Pro
85 90 95
Glu Asn Val Ala Ser Tyr Met Ala Cys Pro Asp Val Asp Gly Ala Leu
100 105 110
Val Gly Gly Ala Ser Leu Glu Ala Glu Ser Phe Leu Ala Leu Leu Asp
115 120 125
Phe Val Lys
130

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

Met Phe Val Glu Ala Cys Lys Ala Val Val Arg Ala Asn Glu Glu Tyr
1 5 10 15
Val Pro Pro Tyr Gly Ile Gly Gly Thr Leu Tyr Leu Arg Pro Leu Leu
20 25 30
Ile Gly Val Gly Asp Ile Ile Gly Val Lys Pro Ala Glu Glu Tyr Ile
35 40 45
Phe Thr Ile Phe Ala Met Pro Val Gly Asn Tyr Phe Lys Gly Gly Leu
50 55 60

Val	Pro	Thr	Asn	Phe	Leu	Ile	Gln	Asp	Glu	Tyr	Asp	Arg	Ala	Ala	Pro
65				70					75						80
Asn	Gly	Thr	Gly	Ala	Ala	Lys	Val	Gly	Gly	Asn	Tyr	Ala	Ala	Ser	Leu
				85				90							95
Leu	Pro	Gly	Lys	Met	Ala	Lys	Ser	Arg	His	Phe	Ser	Asp	Val	Ile	Tyr
				100				105							110
Leu	Asp	Pro	Ser	Thr	His	Thr	Lys	Ile	Glu	Glu	Val	Gly	Ser	Ala	Asn
				115			120								125
Phe	Phe	Gly	Ile	Thr	Ala	Asp	Asn	Glu	Phe	Val	Thr	Pro	Leu	Ser	Pro
				130			135								140
Ser	Ile	Leu	Pro	Ser	Ile	Thr	Lys	Tyr	Ser	Leu	Leu	Tyr	Leu	Ala	Glu
				145			150			155					160
His	Arg	Leu	Gly	Leu	Thr	Pro	Ile	Glu	Gly	Asp	Val	Pro	Ile	Asp	Asn
				165			170								175
Leu	Asp	Arg	Phe	Val	Lys	Ala	Gly	Ala	Cys	Gly	Thr	Ala	Ala	Val	Ile
				180			185								190
Ser	Pro	Ile	Gly	Gly	Ile	Gln	His	Gly	Asp	Asp	Phe	His	Val	Ile	Leu
				195			200								205

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

Met	Val	Met	Ile	Ser	Met	Leu	Phe	Tyr	Ser	Glu	Thr	Glu	Val	Gly	Pro
1					5					10					15
Val	Thr	Arg	Lys	Leu	Tyr	Asn	Glu	Leu	Thr	Gly	Ile	Gln	Phe	Gly	Asp
					20				25						30
Ile	Glu	Ala	Pro	Glu	Gly	Trp	Ile	Val	Lys	Val	Asp				
					35			40							

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

Met Thr Ala Ser Pro Leu Lys Lys Ser Ile Lys Lys Lys Asn Arg Lys
1 5 10 15
Leu Thr Asn Lys Xaa Glu Lys His Met Ser Lys Ile Ile Gly Ile Asp
20 25 30
Leu Gly Thr Thr Asn Ser Ala Val Ala Val Leu Glu Gly Thr Glu Ser
35 40 45
Lys Ile Ile Ala Asn Pro Glu Gly Asn Arg Thr Thr Pro Ser Val Val
50 55 60
Ser Phe Lys Asn Gly Glu Ile Ile Val Gly Asp Ala Ala Lys Arg Gln
65 70 75 80
Ala Val Thr Asn Pro Asp Thr Val Ile Ser Ile Lys Ser Lys Met Gly
85 90 95
Thr Ser Glu Lys Val Ser Ala Asn Gly Lys Glu Tyr Thr Pro Gln Glu
100 105 110
Ile Ser Ala Met Ile Leu Gln Tyr Leu Lys Gly Tyr Ala Glu Asp Tyr
115 120 125
Leu Gly Glu Lys Val Thr Lys Ala Val Ile Thr Val Pro Ala Tyr Phe
130 135 140
Asn Asp Ala Gln Arg Gln Ala Thr Lys Asp Ala Gly Lys Ile Ala Gly
145 150 155 160
Leu Glu Val Xaa Arg Ile Val Asn Glu Pro Thr Ala Ala Ala Leu Ala
165 170 175
Tyr Gly Leu Asp Lys Thr Asp Lys Glu Glu Lys Ile Leu Val Phe Asp
180 185 190
Leu Gly Gly Thr Phe Asp Val Ser Ile Leu Glu Leu Gly Asp Gly
195 200 205
Val Phe Asp Val Leu Ser Thr Ala Gly Asp Asn Lys Leu Gly Gly Asp
210 215 220
Asp Phe Asp Gln Lys Ile Ile Asp His Leu Val Ala Glu Phe Lys Lys
225 230 235 240
Glu Asn Gly Ile Arg Leu Val Tyr
245

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

Met	Lys	Leu	Ile	Val	Asp	Leu	Ile	Tyr	Glu	Gly	Gly	Phe	Lys	Lys	Met
1									10						15
Arg	Gln	Ser	Ile	Ser	Asn	Thr	Ala	Glu	Tyr	Gly	Asp	Tyr	Val	Ser	Gly
									20		25				30
Pro	Arg	Val	Ile	Thr	Glu	Gln	Val	Lys	Glu	Asn	Met	Lys	Ala	Val	Leu
									35		40				45
Ala	Asp	Ile	Gln	Asn	Gly	Lys	Phe	Ala	Asn	Asp	Phe	Val	Asn	Asp	Tyr
									50		55				60
Lys	Ala	Gly	Arg	Pro	Lys	Leu	Thr	Ala	Tyr	Arg	Glu	Gln	Ala	Ala	Asn
									65		70				80
Leu	Glu	Ile	Glu	Lys	Val	Gly	Ala	Glu	Leu	Arg	Lys	Ala	Met	Pro	Phe
									85		90				95
Val	Gly	Lys	Asn	Asp	Asp	Asp	Ala	Phe	Lys	Ile	Tyr	Asn			
									100		105				

(2) INFORMATION FOR SEO ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

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Met Leu Leu Ser Ala Phe His Lys Tyr Glu Asn Gln Leu Asp Lys Val
 1           5           10          15
Arg Phe Ile Gly Leu His Thr Gly His Leu Gly Phe Tyr Thr Asp Tyr
 20          25          30
Arg Asp Phe Glu Leu Asp Lys Leu Val Thr Asn Leu Gln Leu Asp Thr
 35          40          45
Gly Ala Arg Val Ser Tyr Pro Val Leu Asn Val Lys Val Phe Leu Glu
 50          55          60
Asn Gly Glu Val Lys Ile Phe Arg Ala Leu Asn Glu Ala Ser Ile Arg
 65          70          75          80

```

Arg Ser Asp Arg Thr Met Val Ala Asp Ile Val Ile Asn Gly Val Pro
85 90 95
Phe Glu Arg Phe Arg Gly Asp Gly Leu Thr Val Ser Thr Pro Thr Gly
100 105 110
Ser Thr Ala Tyr Asn
115

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

Met Gly Ala Gln Leu Ala Arg Glu Phe Lys His Glu Ala Asp Ile Val
1 5 10 15
Val Gly Val Pro Asn Ser Ser Leu Ser Ala Ala Met Gly Phe Ala Glu
20 25 30
Glu Ser Gly Leu Pro Asn Glu Met Gly Leu Ile Lys Asn Gln Tyr Thr
35 40 45
Gln Arg Thr Phe Ile Gln Pro Thr Gln Glu Leu Arg Glu Gln Gly Val
50 55 60
Arg Met Lys Leu Ser Ala Val Ser Gly Val Val Lys Gly Lys Arg Val
65 70 75 80
Val Met Val Asp Asp Ser Ile Val Arg Gly Thr Thr Ser Arg Arg Ile
85 90 95
Val Gln Leu Leu Lys Glu Ala Gly Ala Thr Glu Val His Val Ala Ile
100 105 110
Gly Ser Pro Ala Leu Ala Tyr Pro Cys Phe Tyr Gly Ile Asp Ile Gln
115 120 125
Thr Arg Gln Glu Leu Ile Ala Ala Asn His Thr Val Glu Glu Thr Arg
130 135 140
Gln Ile Ile Gly Ala Asp Ser Leu Thr Tyr Leu Ser Ile Asp Ser Leu
145 150 155 160
Ile Glu Ser Ile Gly Ile Glu Thr Asp Ala Pro Asn Gly Gly Leu Cys
165 170 175
Val Ala Tyr Phe Asp Gly Asp Tyr Pro Thr Pro Leu Tyr Asp Tyr Glu
180 185 190

Glu Asp Tyr Arg Arg Ser Leu Glu Glu Lys Thr Ser Phe Tyr Lys
195 200 205

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

Met Lys Ile Leu Val Thr Gly Phe Asn Pro Phe Gly Gly Glu Lys Ile
1 5 10 15
Asn Pro Ala Leu Glu Ala Val Lys Leu Leu Pro Ser Glu Ile Asn Gly
20 25 30
Ala Glu Val Arg Trp Val Glu Ile Pro Thr Val Phe Tyr Lys Ser Ser
35 40 45
Glu Val Leu Glu Ala Glu Ile Leu Arg Tyr Gln Pro Asp Ala Val Leu
50 55 60
Cys Ile Gly Gln Ala Gly Gly Arg Thr Gly Leu Thr Pro Glu Arg Val
65 70 75 80
Ala Ile Asn Gln Asp Asp Ala Arg Ile Pro Asp Asn Glu Gly Asn Gln
85 90 95
Pro Ile Asp Thr Pro Ile Arg Ile Asp Gly Ala Ser Ala Tyr Phe Ser
100 105 110
Ser Leu Pro Ile Lys Ala Met Val Gln Ala Asn Lys Lys Glu Gly Leu
115 120 125
Thr Gly Ser Leu Phe Pro Ile Arg Ala Gly Thr Phe Val Cys Ser His
130 135 140
Leu Met Tyr Gln Ala Leu Tyr Leu Val Glu Lys Lys Phe Pro Tyr Val
145 150 155 160
Lys Ala Gly Phe Met His Ile Pro Tyr Met Met Glu Gln Val Val Asn
165 170 175
Arg Pro Thr Thr Pro Thr Met Ser Leu Val Asp Ile Arg Arg Gly Ile
180 185 190
Glu Ala Ala Ile Gly Ala Met Ile Glu His Gly Asp Gln Glu Leu Thr
195 200 205
Leu Val Gly Gly Glu Ile His
210 215

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

Met	Leu	Val	Pro	Lys	Arg	Val	Lys	His	Arg	Arg	Glu	Phe	Arg	Gly	Lys
1						5			10						15
Met	Arg	Gly	Glu	Ala	Lys	Gly	Gly	Lys	Glu	Val	Ala	Phe	Gly	Glu	Tyr
	20							25							30
Gly	Leu	Gln	Ala	Thr	Thr	Ser	His	Trp	Ile	Thr	Asn	Arg	Gln	Ile	Glu
	35						40							45	
Ala	Ala	Arg	Ile	Ala	Met	Thr	Arg	Tyr	Met	Lys	Arg	Gly	Gly	Lys	Val
	50					55			60						
Trp	Ile	Lys	Ile	Phe	Pro	His	Lys	Ser	Tyr	Thr	Ala	Lys	Ala	Ile	Gly
65						70			75						80
Val	Arg	Met	Gly	Ser	Gly	Lys	Gly	Ala	Pro	Glu	Gly	Trp	Val	Ala	Pro
	85							90							95
Val	Lys	Arg	Gly	Lys	Val	Met	Phe	Glu	Ile	Ala	Gly	Val	Ser	Glu	Glu
	100						105							110	
Ile	Ala	Arg	Glu	Ala	Leu	Arg	Leu	Ala	Ser	His	Lys	Leu	Pro	Val	
	115						120							125	

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

Met	Gly	Trp	Trp	Arg	Glu	Thr	Ile	Asp	Ile	Val	Lys	Glu	Asn	Asp	Pro
1						5				10					15

Ala Ala Arg Thr Thr Leu Glu Val Leu Leu Thr Tyr Pro Gly Val Lys
20 25 30
Ala Leu Ala Ala His Arg Leu Ser His Phe Leu Trp Lys Tyr Asp Phe
35 40 45
Lys Leu Leu Ala Arg Met His Ser Gln Phe Trp Arg Phe Trp Thr Gln
50 55 60
Ile Glu Ile His Pro Gly Ala Gln Ile Asp Ser Gly Val Phe Ile Asp
65 70 75 80
His Gly Ser Gly Leu Val Ile Gly Glu Thr Ala Ile Val Glu Lys Gly
85 90 95
Val Leu Leu Tyr His Gly Val Thr Leu Gly Gly Thr Gly Lys Asp Cys
100 105 110
Gly Lys Arg His Pro Thr Val Arg Lys Gly Ala Leu Ile Ser Ala His
115 120 125
Ala Gln Val Ile Gly Pro Val Glu Ile Gly Glu Asn Ala Lys Val Gly
130 135 140
Ala Ala Ala Val Val Val Ala Asp Val Pro Ser Asp Val Thr Val Val
145 150 155 160
Gly Ile Pro Ala Lys Ile Val Arg Leu His Gly Lys Lys Asp Glu Pro
165 170 175
Val Ile His Glu Val Glu Glu Lys Arg Glu Tyr Tyr Val Asn Lys Leu
180 185 190
Glu Gln Ala Lys Asp Ala Ser His Arg Ser Ser Gly Leu
195 200 205

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

Met Leu Phe Tyr Leu Leu Arg Asp Gly Lys Gly Leu Arg Asn Tyr Leu
1 5 10 15
Thr Gln Phe Ile Pro Ser Lys Leu Lys Glu Pro Val Gly Gln Val Leu
20 25 30
Ser Asp Val Asn Gln Gln Leu Ser Asn Tyr Val Arg Gly Gln Val Thr
35 40 45

Val Ala Ile Ile Val Ala Val Met Phe Ile Ile Phe Phe Lys Ile Ile
 50 55 60
 Gly Leu Arg Tyr Ala Val Thr Leu Gly Val Thr Ala Gly Ile Leu Asn
 65 70 75 80
 Leu Val Pro Tyr Leu Gly Ser Phe Leu Ala Met Leu Pro Ala Leu Val
 85 90 95
 Leu Gly Leu Ile Ala Gly Pro Val Met Leu Leu Lys Val Val Ile Val
 100 105 110
 Phe Ile Val Glu Gln Thr Ile Glu Gly Arg Phe Val Ser Pro Leu Ile
 115 120 125
 Leu Gly Ser Gln Leu Asn Ile His Pro Ile Asn Val Leu Phe Val Leu
 130 135 140
 Leu Thr Ser Gly Ser Met Phe Gly Ile Trp Gly Val Leu Leu Gly Ile
 145 150 155 160
 Pro Val Tyr Ala Ser Ala Lys Val Val Ile Ser Ala Ile Phe Glu Trp
 165 170 175
 Tyr Lys Val Val Ser Gly Leu Tyr Glu Leu Glu Gly Glu Val Lys
 180 185 190
 Ser Glu Gln
 195

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

Met Thr Lys Gln Val Pro Lys Phe Thr Lys Asp Thr Ala Gln Leu Tyr
 1 5 10 15
 Thr Cys Lys Trp Leu Leu Tyr Asn Lys Val Thr Lys Met Tyr Asp His
 20 25 30
 Thr Val Val Asn His Ser Val Arg Glu Tyr Ile Thr Asp Ser Ile Ser
 35 40 45
 Thr Asn Thr Ile Glu Glu Thr Gly
 50 55

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

Met Lys Lys Arg Ala Ile Val Ala Val Ile Val Leu Leu Leu Ile Gly
1 5 10 15
Leu Asp Gln Leu Val Lys Ser Tyr Ile Val Gln Gln Ile Pro Leu Gly
20 25 30
Glu Val Arg Ser Trp Ile Pro Asn Phe Val Ser Leu Thr Tyr Leu Gln
35 40 45
Asn Arg Gly Ala Ala Phe Ser Ile Leu Gln Asp Gln Gln Leu Leu Phe
50 55 60
Ala Val Ile Thr Leu Val Val Val Ile Gly Ala Ile Trp Tyr Leu His
65 70 75 80
Lys His Met Glu Asp Ser Phe Trp Met Val Leu Gly Leu Thr Leu Ile
85 90 95
Ile Ala Gly Gly Leu Gly Asn Phe Ile Asp Arg Val Ser Gln Gly Phe
100 105 110
Val Val Asp Met Phe His Leu Asp Phe Ile Asn Phe Ala Ile Phe Asn
115 120 125
Val Ala Asp Asn Tyr Leu Thr Val Gly Val Ile Ile Leu Leu Ile Ala
130 135 140
Met Leu Lys Glu Glu Ile Asn Gly Asn
145 150

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

Met Gly Ala Tyr Tyr Leu Val Met Gln Ser Leu Ser Tyr Leu Glu Tyr
 1 5 10 15
 Glu Gln Gly Ile Gln Ser Thr Thr Val Arg His Leu Ile Leu Val Phe
 20 25 30
 Tyr Leu Leu Phe Phe Met Gly Gly Ile Lys Lys Leu Asp Thr Tyr Leu
 35 40 45
 Lys Glu Lys Leu Gln Glu Glu Leu Asn Gln Glu Gln Thr Leu Arg Tyr
 50 55 60
 Arg Asp Met Glu Arg Tyr Ser Arg His Ile Glu Glu Leu Tyr Lys Glu
 65 70 75 80
 Ile Arg Ser Phe Arg His Asp Tyr Thr Asn Leu Leu Thr Thr Tyr Val
 85 90 95
 Trp Ala Leu Lys Arg Arg Ile Trp Ser Arg
 100 105

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

Met His Val Arg Met Ile Pro Lys Ser Thr Pro Asp Thr Lys Phe Ala
 1 5 10 15
 Asp Val Ala Thr His Gln Pro Glu Tyr Ser Arg Asp Asn Val Ala Gly
 20 25 30
 Thr Ile Val Gly Phe Trp Thr Pro Glu Ile Phe His Gly Val Ser Val
 35 40 45
 Ala Gly Tyr His Leu His Phe Ile Ser Asp Asp Leu Thr Phe Gly Gly
 50 55 60
 His Val Met Asp Phe Val Ile Lys Glu Gly Ile Ile Glu Val Gly Ala
 65 70 75 80
 Val Asp Gln Leu Asp Gln Arg Phe Pro Val Gln Asp Arg Gln Tyr Leu
 85 90 95
 Phe Ala Lys Phe Asn Val Asp Glu Met Lys Lys Asp Ile Glu Lys Ala
 100 105 110
 Glu

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

Met Ala Val Ala Lys Gly Lys Leu Thr Ile Ile Ala His Val Ala Cys
1 5 10 15
Asn Asn Thr Lys Asp Ser Met Glu Leu Ala Arg His Ala Glu Ser Leu
20 25 30
Gly Val Asp Ala Ile Ala Thr Asp Ser Thr Asn Leu Phe Pro Leu Ala
35 40 45
Arg Ile Thr Gln Leu Pro Asn Thr Gly Thr Ile Ser Val Leu Gln Leu
50 55 60
Gln Thr Gln Thr Thr
65

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

Met Gly Glu Thr Gln Ile Ile Asp Gly Leu Asp Pro Glu Tyr Lys Lys
1 5 10 15
Arg Phe Met His His Tyr Asn Phe Pro Gln Tyr Ser Val Gly Glu Thr
20 25 30
Gly Arg Tyr Gly Ala Pro Gly Arg Arg Glu Ile Gly His Gly Ala Leu
35 40 45
Gly Glu Arg Ala Leu Ala Gln Val Leu Pro Ser Leu Glu Glu Phe Pro
50 55 60

Tyr Ala Ile Arg Leu Val Ala Glu Val Leu Glu Ser Asn Gly Ser Ser
 65 70 75 80
 Ser Gln Ala Ser Ile Cys Ala Gly Thr Leu Ala Leu Met Ala Gly Gly
 85 90 95
 Val Pro Ile Lys Ala Pro Val Ala Gly Ile Ala Met Gly Leu Ile Ser
 100 105 110
 Asp Gly Asn Asn Tyr Thr Val Leu Thr Asp Ile Gln Gly Leu Glu Asp
 115 120 125
 His Phe Gly Asp Met Asp Phe Lys Val Ala Gly Thr Arg Asp Gly Ile
 130 135 140
 Thr Ala Leu Gln Met Asp Ile Lys Ile Gln Gly Ile Thr Ala Glu Ile
 145 150 155 160
 Leu Thr Glu Ala Leu Ala Gln Ala Lys Lys Ala Arg Phe Glu Ile Leu
 165 170 175
 Asp Val Ile Glu Ala Thr Ile Pro Glu Val Arg Pro Glu Leu Ala Pro
 180 185 190
 Thr Ala Pro Lys Ile Asp Thr Ile Lys Ile Asp Val Asp Lys Ile Lys
 195 200 205
 Ile Val Ile Gly Lys Gly Glu Thr Ile Asp Lys Ile Ile Ala Glu
 210 215 220
 Thr Gly Val Lys Ile Asp Ile Asp Glu Glu Xaa Asn Val Phe Tyr Leu
 225 230 235 240
 Leu Leu Val Asp Gln Asn Ala Ile Asn Pro Cys Pro Lys Lys Leu Leu
 245 250 255
 Leu Val Trp Phe Arg Glu Pro Lys Trp Met Lys Phe Thr Val Leu Asn
 260 265 270
 Arg Ser Tyr Arg Glu Phe Gly Ala Phe Val Thr Leu
 275 280

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

Met Ile Asn Asn Val Val Leu Val Gly Arg Met Thr Arg Asp Ala Glu
 1 5 10 15

Leu	Arg	Tyr	Thr	Pro	Ser	Asn	Val	Ala	Val	Ala	Thr	Phe	Thr	Leu	Ala
20							25				30				
Val	Asn	Arg	Thr	Phe	Lys	Ser	Gln	Asn	Gly	Glu	Arg	Glu	Ala	Asp	Phe
	35					40				45					
Ile	Asn	Val	Val	Met	Trp	Arg	Gln	Gln	Ala	Glu	Asn	Leu	Ala	Asn	Trp
	50						55			60					
Ala	Lys	Lys	Gly	Ser	Leu	Ile	Gly	Val	Thr	Gly	Arg	Ile	Gln	Thr	Arg
	65				70				75			80			
Ser	Tyr	Asp	Asn	Gln	Gln	Gly	Gln	Arg	Val	Tyr	Val	Thr	Glu	Val	Val
		85					90			95					
Ala	Glu	Asn	Phe	Gln	Met	Leu	Glu	Ser	Arg	Ser	Val	Arg	Glu	Gly	His
		100					105			110					
Thr	Gly	Gly	Ala	Tyr	Ser	Ala	Pro	Thr	Ala	Asn	Tyr	Ser	Ala	Pro	Thr
	115						120			125					
Asn	Ser	Val	Pro	Asp	Phe	Ser	Arg	Asn	Glu	Asn	Pro	Phe	Gly	Ala	Thr
	130					135				140					
Asn	Pro	Leu	Asp	Ile	Ser	Xaa	Asp	Asp	Leu	Pro	Phe				
	145					150			155						

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

Met	Asp	Leu	Val	Arg	Ile	Leu	Lys	Glu	Pro	Arg	Asn	Ala	Leu	Val	Lys
1						5				10			15		
Gln	Tyr	Gln	Thr	Leu	Leu	Ser	Tyr	Asp	Asp	Val	Glu	Leu	Glu	Phe	Asp
				20				25			30				
Asp	Glu	Ala	Leu	Gln	Glu	Ile	Ala	Asn	Lys	Ala	Ile	Glu	Arg	Lys	Thr
				35				40			45				
Gly	Ala	Arg	Gly	Leu	Arg	Ser	Ile	Ile	Glu	Glu	Thr	Met	Leu	Asp	Val
				50				55			60				
Met	Phe	Glu	Val	Pro	Ser	Gln	Glu	Asn	Val	Lys	Leu	Val	Arg	Ile	Thr
	65						70			75			80		
Lys	Glu	Thr	Val	Asp	Gly	Thr	Asp	Lys	Pro	Ile	Leu	Glu	Thr	Ala	
				85				90			95				

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

Met	Thr	Glu	Ala	Gly	Tyr	Val	Gly	Glu	Asp	Val	Glu	Asn	Ile	Leu	Leu
1															15
Lys	Leu	Leu	Gln	Val	Ala	Asp	Phe	Asn	Ile	Glu	Arg	Ala	Glu	Arg	Gly
															30
Ile	Ile	Tyr	Val	Asp	Glu	Ile	Asp	Lys	Ile	Ala	Lys	Lys	Ser	Glu	Asn
															45
Val	Ser	Ile	Thr	Arg	Asp	Val	Ser	Gly	Glu	Gly	Val	Gln	Gln	Ala	Leu
															50
Leu	Lys	Ile	Ile	Glu	Gly	Thr	Val	Ala	Ser	Val	Pro	Pro	Gln	Gly	Gly
															60
Arg	Lys	His	Pro	Gln	Gln	Val	Asp	Asp	Ser	Ser	Gly	Tyr	Lys	Lys	Tyr
															85
Pro	Leu	His	Arg	Gly	Trp	Cys	Phe								90
															100

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

Met	Trp	Pro	Arg	Glu	Ser	Arg	Ser	Cys	Arg	Leu	Thr	Lys	Val	Lys	Ile
1															15
															5
															10

Cys Gly Leu Ser Thr Lys Glu Ala Val Glu Thr Ala Val Ser Ala Gly
 20 25 30
 Ala Asp Tyr Ile Gly Phe Val Phe Ala Pro Ser Lys Arg Gln Val Thr
 35 40 45
 Leu Glu Glu Ala Ala Glu Leu Ala Lys Leu Ile Pro Ala Asp Val Lys
 50 55 60
 Lys Val Gly Val Phe Val Ser Pro Ser Arg Val Glu Leu Leu Glu Ala
 65 70 75 80
 Ile Asp Lys Val Gly Leu Asp Leu Val Gln Val His Gly Gln Val Ala
 85 90 95
 Asp Asp Leu Phe Glu Asn Leu Pro Cys Ala Ser Ile Gln Ala Val Gln
 100 105 110
 Val Asp Gly Asn Gly His Val Pro Asn Ser Gln Ala Asp Tyr Leu Leu
 115 120 125
 Phe Asp Ala Pro Val Ala Gly Ser Gly Gln Ser Phe Asp Trp Gly Gln
 130 135 140
 Leu Asp Thr Thr Gly Leu Ala Gln Pro Phe Phe Ile Ala Gly Gly Leu
 145 150 155 160
 Asn Glu Asp Asn Val Val Lys Ala Ile Gln His Phe Thr Pro Tyr Ala
 165 170 175
 Val Asp Val Ser Ser Gly Val Glu Thr Asp Gly Gln Lys Asp His Glu
 180 185 190
 Lys Ile Arg Arg Phe Ile Glu Arg Val Lys His Gly Ile Ser Gly Thr
 195 200 205
 Lys

(2) INFORMATION FOR SEQ ID NO:288:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

Met Asn Cys Glu Ala Val Ala Leu Gly Ser Phe Cys Glu Leu Lys Ser
 1 5 10 15
 Arg Arg Gly Lys Lys Gln Lys Gly Glu Ile Leu Met Ala Val Ile Ser
 20 25 30

Met Lys Gln Leu Leu Glu Ala Gly Val His Phe Gly His Gln Thr Arg
35 40 45
Arg Trp Asn Pro Lys Met Ala Lys Tyr Ile Phe Thr Glu Arg Asn Gly
50 55 60
Ile His Val Ile Asp Leu Gln Gln Thr Val Lys Tyr Ala Asp Gln Ala
65 70 75 80
Tyr Xaa Phe Met Arg Asp Ala Ala Asn Asp Ala Val Val Leu Phe
85 90 95
Val Gly Thr Lys Lys Thr Ser Ser
100

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

Met Val Asp Thr Asn Thr Asp Pro Asp Asp Ile Asp Val Ile Ile Pro
1 5 10 15
Ala Asn Asp Asp Ala Ile Arg Ala Val Lys Leu Ile Thr Ala Lys Leu
20 25 30
Ala Asp Ala Ile Ile Glu Gly Arg Gln Gly Glu Asp Ala Val Ala Val
35 40 45

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

Met Glu Glu Leu Gly Gln Ser Tyr Gly Tyr Leu Leu Tyr Arg Thr Glu
1 5 10 15

Thr Asn Trp Asp Ala Glu Glu Glu Arg Leu Arg Ile Ile Asp Gly Arg
 20 25 30
 Asp Arg Ala Gln Leu Tyr Val Asp Gly Gln Trp Val Lys Thr Gln Tyr
 35 40 45
 Gln Thr Glu Ile Gly Glu Asp Ile Phe Tyr Gln Gly Lys Lys Lys Gly
 50 55 60
 Leu Ser Arg Leu Asp Ile Leu Ile Glu Asn Met Gly Arg Val Asn Tyr
 65 70 75 80
 Gly His Lys Phe Leu Ala Asp Thr Gln Arg Lys Gly Ile Arg Thr Gly
 85 90 95
 Val Cys Lys Asp Leu His Phe Leu Leu Asn Trp Lys His Tyr Pro Leu
 100 105 110
 Pro Leu Asp Asn Pro Glu Lys Ile Asp Phe Ser Lys Gly Trp Thr Gln
 115 120 125
 Gly Gln Pro Ala Phe Tyr Ala Tyr Asp Phe Thr Val Glu
 130 135 140

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

Met Gly Lys Glu Lys Val Trp Leu Pro Arg Lys Gln Gly Leu Pro Gly
 1 5 10 15
 Leu Ala Tyr Tyr Val Ile Glu Val Ala His Lys Glu Glu Leu Leu Thr
 20 25 30
 Ile Ala Gln Arg Ala Gln Glu Val Asp Val Pro Ile Lys Trp Met Thr
 35 40 45
 Ser Ser Gln Leu Glu Ile Thr Asp Ser Asp Gly Ile Val Thr Cys Ile
 50 55 60
 Arg Leu Ala Arg
 65

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

Met Asn Lys Lys Gln Trp Leu Gly Leu Gly Leu Val Ala Val Ala Ala
1 5 10 15
Val Gly Leu Ala Ala Cys Gly Asn Arg Ser Ser Arg Asn Ala Ala Ser
20 25 30
Ser Ser Asp Val Lys Thr Lys Ala Ala Ile Val Thr Asp Thr Gly Gly
35 40 45
Val Asp Asp Lys Ser Phe Asn Gln Ser Ala Trp Glu Val Ala Gly Leu
50 55 60
Gly
65

(2) INFORMATION FOR SEQ ID NO:293:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 157 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

Met Ser Gln Trp Asp Arg Lys Leu Asp Ala Arg Leu Ala Gln Ala Val
1 5 10 15
Val Ser Ile Asn Ala Phe Lys Gly Val Glu Phe Gly Leu Gly Phe Glu
20 25 30
Ala Gly Tyr Arg Lys Gly Ser Gln Val Met Asp Glu Ile Leu Trp Ser
35 40 45
Lys Glu Asp Gly Tyr Thr Arg Arg Thr Asn Asn Leu Gly Gly Phe Glu
50 55 60
Gly Gly Met Thr Asn Gly Gln Pro Ile Val Val Arg Gly Val Met Lys
65 70 75 80
Pro Ile Pro Thr Leu Tyr Lys Pro Leu Met Ser Val Asp Ile Glu Thr
85 90 95

His Glu Pro Tyr Lys Ala Thr Val Glu Arg Ser Asp Pro Thr Ala Leu
100 105 110
Pro Ala Ala Gly Met Val Met Glu Ala Val Val Ala Thr Val Leu Ala
115 120 125
Gln Glu Ile Leu Glu Lys Phe Ser Ser Asp Asn Leu Glu Glu Leu Lys
130 135 140
Glu Ala Val Ala Lys His Arg Asp Tyr Thr Lys Asn Tyr
145 150 155

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

Met Glu Asp Ser Asn Ser Phe Met Leu Ser His Gln Met Glu Thr Ile
1 5 10 15
Leu Lys Glu Ala Gly Phe Thr Lys Ala Val Ser Tyr Phe Ile Leu Glu
20 25 30
Leu Lys Asp Pro Ser Gln Thr Lys Val Val Thr Glu Glu Leu Gln Lys
35 40 45
Asn Lys Lys Tyr Thr Val Leu Ser
50 55

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

Met Gly Lys Lys Arg Trp Ala Arg Asn Gly Phe Glu Ser Asn Asp Ala
1 5 10 15

Ser Tyr Ala Gln Val Val Ser Leu Tyr Asp Asp Thr Ser Ile Ser Val
20 25 30
Ser Asn Asn Glu Thr Asp Lys Val Leu Ala Gly Ser Leu Tyr Thr Asp
35 40 45
Thr Asn Glu Gln Gly Leu Thr Ile Pro Ser Ser Phe Thr Lys Lys Leu
50 55 60
Glu
65

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

Met Ala Met Glu Ser Gly Ala Thr Ala Val Val Ala Glu Arg Gly Gln
1 5 10 15
Glu Arg Ile Thr Lys Val Arg Glu Ile Leu Gly Gly Ala Asp Ala
20 25 30
Ala Leu Glu Cys Val Gly Thr Glu Ala Ala Ile Glu Gln Ala Leu Gly
35 40 45
Val Leu His Asn Gly Gly Arg Met Gly Phe Val Gly Val Pro His Tyr
50 55 60
Asn Asn Arg Ala Leu Gly Ser Thr Phe Met Gln Asn Ile Ser Val Ala
65 70 75 80
Gly Gly Ala Ala Ser Ala Thr Thr Tyr Asp Lys Gln Phe Leu Leu Lys
85 90 95
Ala Val Leu Asp Gly Asp Ile Asn Pro Gly Arg Val Phe Thr Ser Ser
100 105 110
Tyr Lys Leu Glu Asp Ile Asp Gln Ala Tyr Lys Asp Met Asp Glu Arg
115 120 125
Lys Thr Ile Lys Ser Met Ile Val Ile Glu
130 135

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

Met Lys Gln Val Val Asp Tyr Phe Leu Ser Gln Gly Met Asp Arg Ile
1 5 10 15
Gly Ile Leu Thr Gly Leu Glu Glu Thr Thr Asp Gln Glu Glu Ile Ile
20 25 30
Gln Asp Lys Arg Leu Glu Asn Phe Lys Asn Tyr Ser Gln Ala Arg Gly
35 40 45
Ile Tyr His Asp Glu Leu Val Phe Gln Gly Arg Phe Thr Ala Gln Ser
50 55 60
Gly Tyr Asp Leu Met Lys Glu Ala Ile Gln Ser Leu Gly Asp Gln Leu
65 70 75 80
Pro Pro Ala Phe Phe Ala Ala Ser Asp Ser Leu Ala Ile Gly Ala Leu
85 90 95
Arg Ala Leu Gln Glu Ala Gly Ile Ser Leu Pro Asp Arg Val Ser Leu
100 105 110
Ile Phe Leu Leu Thr Thr Leu Ser Leu Thr Lys Gln Val Tyr Pro Pro
115 120 125
Leu Ser
130

(2) INFORMATION FOR SEQ ID NO:298:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

Met Ala Lys Val Thr Ile Met Leu Ala Cys Ala Ala Gly Met Ser Thr
1 5 10 15
Ser Leu Leu Val Thr Lys Met Gln Lys Ala Ala Glu Asp Lys Gly Leu
20 25 30

Asp Ala Glu Ile Phe Ala Val Pro Ala Pro Glu Ala Glu Glu Ile Val
 35 40 45
 Ala Thr Lys Glu Val Asn Val Leu Leu Leu Gly Pro Gln Val Arg Tyr
 50 55 60
 Leu Leu Gly Asp Phe Gln Glu Lys Leu Lys Asp Arg Gln Ile Pro Val
 65 70 75 80
 Ala Val Ile Pro Met Thr Asp Tyr Gly Met Met Asn Gly Ser Lys Val
 85 90 95
 Leu Asp Leu Ala Glu Ser Leu Leu Asp
 100 105

(2) INFORMATION FOR SEQ ID NO:299:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

Met His Gly Ala Gly Val Asn Glu Pro Val Ala Glu Leu Ser Val Ala
 1 5 10 15
 Glu Gln Leu Leu Glu Ala Gly Ala Asp Val Ile Leu Val Pro Ala Val
 20 25 30
 Gly Thr Val Pro Ala Phe His Asp Gln Glu Leu Arg Glu Val Val Asp
 35 40 45
 Leu Val His Ser Lys Gly Gly Leu Val Leu Ser Ala Ile Gly Thr Ser
 50 55 60
 Gln Glu Thr Ser Asp Thr Asp Thr Ile Lys Glu Ile Ala Leu Arg Asn
 65 70 75 80
 Lys Ile Cys Gly Val Asp Ile Gln His Ile Gly Asp Ala Gly Tyr Gly
 85 90 95
 Gly Leu Ala Thr Val Asp Asn Ile Tyr Ala Leu Ser Lys Ala Ile Arg
 100 105 110
 Gly Val Arg His Thr Val Ser Arg Leu Ala Arg Ser Val Asn Arg
 115 120 125

(2) INFORMATION FOR SEQ ID NO:300:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 236 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

Met Ser Ala Ile Asn Leu Ala Ser Val Pro Lys Glu Ser Leu Thr Gln
1 5 10 15
Val Leu Pro Arg Asp Leu His Ala Glu Tyr Phe Ala Val Leu Ala Ser
20 25 30
Ile Ala Thr Ser Ile Glu Arg Met Ala Thr Glu Ile Arg Gly Leu Gln
35 40 45
Lys Ser Glu Gln Arg Glu Val Glu Glu Phe Phe Ala Lys Gly Gln Lys
50 55 60
Gly Ser Ser Ala Met Pro His Lys Arg Asn Pro Ile Gly Ser Glu Asn
65 70 75 80
Met Thr Gly Leu Ala Arg Val Ile Arg Gly His Met Ile Thr Ala Tyr
85 90 95
Glu Asn Val Ala Leu Trp His Glu Arg Asp Ile Ser His Ser Ser Ala
100 105 110
Glu Arg Ile Ile Thr Pro Asp Thr Thr Ile Leu Ile Asp Tyr Met Leu
115 120 125
Asn Arg Phe Gly Asn Ile Val Lys Asn Leu Thr Val Phe Pro Glu Asn
130 135 140
Met Ile Arg Asn Met Asn Ser Thr Phe Gly Leu Ile Phe Ser Gln Arg
145 150 155 160
Ala Met Leu Thr Leu Ile Glu Lys Gly Met Thr Arg Glu Gln Ala Tyr
165 170 175
Asp Leu Val Gln Pro Lys Thr Ala Tyr Ser Trp Asp Asn Gln Val Asp
180 185 190
Phe Lys Pro Leu Leu Glu Ala Asp Ser Glu Val Thr Ser Arg Leu Thr
195 200 205
Gln Glu Glu Ile Asp Glu Ile Phe Asn Pro Val Tyr Tyr Thr Lys Arg
210 215 220
Val Asp Asp Ile Phe Glu Arg Leu Gly Leu Gly Asp
225 230 235

(2) INFORMATION FOR SEQ ID NO:301:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 97 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

Met Leu Asn Leu Thr His Val Thr Leu Lys Thr Arg Gln Val Ile Leu
1 5 10 15
Gln Asp Ala Asp Phe Thr Phe Lys Lys Gly Arg Ile Tyr Gly Leu Leu
20 25 30
Ala Ile Asn Gly Ser Gly Lys Thr Thr Leu Phe Arg Ala Met Ser Lys
35 40 45
Leu Leu Pro Leu Ser Ser Gly His Ile Ala Val Pro Pro Ser Leu Phe
50 55 60
Tyr Tyr Glu Ser Val Glu Trp Leu Asp Gly Asn Leu Ser Gly Met Asp
65 70 75 80
Tyr Leu Arg Leu Ile Lys Lys His Leu Glu Val Arg Pro Lys Leu Glu
85 90 95
Arg

(2) INFORMATION FOR SEQ ID NO:302:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

Met Tyr Thr Leu Gly Gln Pro Asn Glu Leu Ala Ala Glu Phe Leu Asn
1 5 10 15
Phe Val Leu Ser Asp Glu Thr Gln Glu Gly Ile Val Lys Gly Leu Lys
20 25 30
Tyr Ile Pro Ile Lys Glu Met Lys Val Glu Lys Asp Ala Ala Gly Thr
35 40 45
Val Thr Val Leu Glu Gly Arg Gln
50 55

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

Met	Asn	Gln	Glu	Glu	Leu	Ala	Lys	Lys	Met	Leu	Leu	Pro	Ser	Lys	Asn	
1				5					10						15	
Ser	Arg	Leu	Glu	Glu	Lys	Leu	Gly	Lys	Gly	Leu	Thr	Phe	Ala	Cys	Leu	Ser
					20					25					30	
Leu	Ile	Val	Ile	Leu	Val	Ala	Met	Ile	Leu	Val	Phe	Val	Ala	Gln	Lys	
				35				40						45		
Gly	Leu	Ser	Thr	Phe	Phe	Val	Asn	Gly	Val	Asn	Ile	Phe	Asp	Phe	Leu	
				50				55			60					
Leu	Gly	Gly	Thr	Trp	Asn	Pro	Ser	Ser	Lys	Glu	Phe	Gly	Ala	Leu	Pro	
	65				70				75					80		
Met	Ile	Leu	Gly	Ser	Phe	Ile	Val	Thr	Ile	Leu	Ser	Ala	Leu	Ile	Ala	
					85				90					95		
Thr	Pro	Phe	Ala	Ile	Gly	Ala	Ala	Val	Phe	Met	Thr	Glu	Val	Ser	Pro	
					100				105			110				
Lys	Gly	Ala	Lys	Ile	Leu	Gln	Pro	Ala	Ile	Glu	Leu	Leu	Val	Gly	Ile	
				115				120			125					
Pro	Ser	Val	Val	Tyr	Gly	Phe	Ile	Gly	Leu	Gln	Val	Val	Val	Pro	Phe	
				130				135			140					
Val	Arg	Ser	Val	Phe	Gly	Gly	Thr	Gly	Phe	Gly	Ile	Leu	Ser	Gly	Ile	
	145				150					155				160		
Ser	Val	Leu	Phe	Val	Met	Ile	Leu	Pro	Thr	Val	Thr	Phe	Met	Thr	Thr	
					165				170					175		
Asp	Ser	Leu	Arg	Ala	Val	Pro	Xaa	Leu	Leu	Ser						
					180			185								

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

Met Thr Glu Ile Arg Leu Glu His Val Ser Tyr Ala Tyr Gly Gln Glu
1 5 10 15
Arg Ile Leu Glu Asp Ile Asn Leu Gln Val Thr Ser Gly Glu Val Val
20 25 30
Ser Ile Leu Gly Pro Ser Gly Val Gly Lys Thr Thr Leu Phe Asn Leu
35 40 45
Ile Ala Gly Ile Leu Glu Val Gln Ser Gly Arg Ile Val Leu Asp Gly
50 55 60
Glu Glu Asn Pro Lys Gly His Val Ser Tyr Met Leu Gln Lys Asp Leu
65 70 75 80
Leu Leu Glu His Lys Thr Val Leu Gly Asn Ile Ile Leu Pro Leu Leu
85 90 95
Ile Gln Lys Val Asp Lys Ala Glu Ala Ile Ser Arg Ala Asp Lys Ile
100 105 110
Leu Ala Thr Phe Gln Leu Thr Ala Val Arg Asp Lys Tyr Pro His Glu
115 120 125
Leu Ser Gly Gly Met Arg Gln Arg Val Ala Leu Leu Arg Thr Tyr Leu
130 135 140
Phe Gly His Lys Leu Phe Leu Leu Asp Glu Ala Phe Ser Ala Leu Asp
145 150 155 160
Glu Met Thr Lys Met Glu Leu His Ala Trp Tyr Leu Glu Ile His Lys
165 170 175
Gln Leu Gln Leu Thr Thr Leu Ile Xaa Thr His Ser Ile Glu Glu Ala
180 185 190
Leu Xaa Leu Ser Asp Arg Ile Tyr Ile Leu Xaa Asn Xaa Pro Gly Gln
195 200 205
Ile Val Ser Glu Ile Lys Leu Asp Trp Ser Glu Asp Glu Asp Xaa Glu
210 215 220
Val Xaa Lys Ile Ala Xaa Lys Arg Gln Ile Leu Ala Glu Leu Gly Leu
225 230 235 240
Asp Lys

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

Met Glu His Pro Xaa Glu Ala Ala Asp Ile Leu Ile Lys Asn Ala Pro
1 5 10 15
Glu Leu Lys Glu Lys Arg Asp Phe Val Ile Glu Ser Gln Lys Tyr Leu
20 25 30
Ser Lys Glu Tyr Ala Ser Asp Lys Glu Lys Trp Gly Gln Phe Asp Ala
35 40 45
Ala Arg Trp Asn Ala Phe Tyr Lys Trp Asp Lys Glu Asn Gly Ile Leu
50 55 60
Lys Glu Asp Leu Thr Asp Lys Gly Phe Thr Asn Glu Phe Val Lys
65 70 75

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

Met Val Tyr Thr Ser Leu Ser Ser Lys Asp Gly Asn Tyr Pro Tyr Gln
1 5 10 15
Leu Asn Ile Ala His Leu Tyr Gly Asn Leu Met Asn Thr Tyr Gly Asp
20 25 30
Asn Gly Asn Ile Leu Met Leu Lys Tyr Val Ala Glu Lys Leu Gly Thr
35 40 45
His Val Thr Val Asp Ile Val Ser Leu His Asp Asp Phe Asp Glu Asn
50 55 60
His Tyr Asp Ile Ala Phe Phe Gly Gly Gln Asp Phe Glu Gln Ser
65 70 75 80
Ile Ile Ala Asp Asp Leu Pro Ala Lys Lys Glu Ser Ile Asp Asn Tyr
85 90 95
Ile Gln Asn Asp Gly Val Val Leu Ala Ile Cys Gly Gly Phe Gln Leu
100 105 110
Leu Gly Gln Tyr Tyr Val Glu Ala Ser Gly Lys Arg Ile Glu Gly Leu
115 120 125

Gly Val Met Gly His Tyr Thr Leu Asn Gln Thr Asn Asn Arg Phe Ile
130 135 140
Gly Asp Ile Lys Ile His Asn Glu Arg Phe Arg
145 150 155

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

Met His Gln His Ser Pro His Thr Ala Ser Tyr Thr Ser Ser Arg Asp
1 5 10 15
Ala Met Ser Lys Tyr Pro Glu Arg Cys Thr Thr Val Gly Leu Arg Leu
20 25 30
Asn Glu Glu Ser Asp Phe Glu Leu Tyr Ala Pro Tyr Gly Leu Glu Asp
35 40 45
Ile Leu Asn Phe Lys Phe Val Gln Leu Leu Ile Ser
50 55 60

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

Met Phe Glu Ile Phe Asn Met Gly Val Gly Leu Met Leu Ala Val Ser
1 5 10 15
Pro Glu Asn Val Glu Arg Val Lys Glu Leu Leu Asp Glu Ala Val Tyr
20 25 30
Glu Ile Gly Arg Ile Val Lys Lys Glu Asn Glu Ser Val Ile Ile Lys
35 40 45

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

Met	Met	Val	Lys	Lys	His	Tyr	Phe	Lys	Asp	Asn	Glu	Glu	Asp	Ser	Lys
1															15
Met	Arg	Arg	Ile	Leu	Leu	Leu	Val	Ala	Val	Leu	Leu	Met	Ile	Pro	Ser
	20													30	
Phe	Ile	Ser	Ala	Thr	Thr	Leu	Val	Arg	Glu	Thr	Leu	Lys	Lys	Glu	Ser
	35													45	
Leu	Lys	Lys	Phe	Ile	Ser	Glu	Gln	Phe	Gln	Gly	His	Asn	Ile	Leu	Lys
	50													60	
Lys	Thr	Tyr	Ser	Lys	Lys	Thr	His	Thr	Leu	Lys	Leu	Thr	Ile	Ser	Gly
	65													80	
Asn	Tyr	Leu	Thr	Glu	Glu	Glu	Leu	Asp	Met	Ile	Ser	Ser	Lys	Arg	Gly
	85													95	
Asp	Tyr	Gly	Leu	Ser	Asp	Val	Ser	Val	Gln	Val	Ser	Gln	Leu	Ser	Asp
	100													110	
Ser	Glu	Gln	Leu	Ser	Lys	Glu	Glu	Leu	Val	Glu	Tyr	Phe	Phe	Gln	Tyr
	115													125	
Ile	Lys	Asp	Lys	Glu	Ala	Lys	Glu	Lys	Glu	Lys	Ala	Asn	Lys	Phe	Tyr
	130													140	
Thr	Glu	Ser	Glu	Glu	Gln										
	145														
	150														

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

Met Ser Ile Glu Pro Arg Arg Arg Trp Arg Asn Ser Thr Val Cys Leu
1 5 10 15
Glu Ala Glu Leu Tyr Gln Glu Ser Leu Val Leu Ile Gly Gly Asp Pro
20 25 30
Gly Ile Gly Lys Ser Thr Leu Leu Gln Val Ser Thr Gln Leu Ser
35 40 45
Gln Val Gly Thr Val Leu Tyr Val Ser Gly Glu Glu Ser Ala Gln Gln
50 55 60
Ile Lys Leu Arg Ala Glu Arg Leu Gly Asp Phe Asp Ser Glu Phe Tyr
65 70 75 80
Leu Tyr Ala Glu Thr Asn Met Gln Ser Val Arg Ala Glu Val Val Ala
85 90 95
Tyr Pro Ala Arg Leu Ser His Tyr
100

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

Met Ala Thr Lys Gln Lys Glu Val Thr Thr Phe Asp Val Gln Val Ala
1 5 10 15
Glu Phe Ile Arg Asn His Lys Gln Lys Gly Thr Ala Thr Asp Asp Glu
20 25 30
Ile Asn Ala Ser Leu Val Ile Pro Phe Thr Leu Asp Ala Asp Gly Ile
35 40 45
Glu Asp Leu Leu Gln Arg Ile Gln Asp Ala Gly Ile Ser Ile Thr Asp
50 55 60
Asn Glu Gly Asn Pro Ser Ala Arg Val Leu Ser Asn Glu Glu Glu Pro
65 70 75 80
Glu Leu Ser Asp Glu Asp Leu Ile Gly Ser Thr Ser Ala Lys Val Asn
85 90 95
Asp Pro Val Arg Met Tyr Leu Lys Glu Ile Gly Val Val Pro Leu Leu
100 105 110

Thr Asn Glu Glu Glu Lys Glu Leu Ala Leu Ala Val Glu Ala Gly Asp
 115 120 125
 Ile Glu Ala Lys Gln Arg Leu Ala Glu Ala Asn Leu Arg Leu Val Val
 130 135 140
 Ser Ile Ala Lys Arg Tyr Val Gly Arg Gly Xaa Gln Ser Leu Thr
 145 150 155

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

Met Met Leu Lys Pro Ser Ile Asp Thr Leu Leu Asp Lys Val Pro Ser
 1 5 10 15
 Lys Tyr Ser Leu Val Ile Leu Glu Ala Lys Arg Ala His Glu Leu Glu
 20 25 30
 Ala Gly Ala Pro Ala Thr Gln Gly Phe Lys Ser Glu Lys Ser Thr Leu
 35 40 45
 Arg Ala Leu Glu Glu Ile Glu Ser Gly Asn Val Thr Ile His Pro Asp
 50 55 60
 Pro Glu Gly Lys Arg Glu Ala Val Arg Arg Arg Ile Glu Glu Glu Lys
 65 70 75 80
 Arg Arg Lys Glu Glu Glu Lys Lys Ile Lys Glu Gln Ile Ala Lys
 85 90 95
 Glu Lys Glu Asp Gly Glu Lys Ile
 100

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

Met	Ile	Arg	Gln	Gly	Gln	Met	Leu	Glu	Tyr	Ala	Glu	Tyr	Val	Gly	Asn
1				5				10					15		
Tyr	Tyr	Gly	Thr	Pro	Leu	Thr	Tyr	Val	Asn	Glu	Thr	Leu	Asp	Lys	Gly
				20				25					30		
Ile	Asp	Val	Phe	Leu	Glu	Ile	Glu	Val	Gln	Gly	Ala	Leu	Gln	Val	Lys
				35				40					45		
Lys	Lys	Val	Pro	Asp	Ala	Val	Phe	Ile	Phe	Leu	Thr	Pro	Pro	Asp	Leu
				50				55					60		
Asp	Glu	Leu	Gln	Glu	Arg	Leu	Val	Gly	Arg	Gly	Thr	Asp	Ser	Ala	Glu
				65				70					75		80
Val	Ile	Ala	Gln	Arg	Ile	Glu	Lys	Ala	Lys	Glu	Glu	Ile	Ala	Leu	Met
				85				90					95		
Arg	Glu	Tyr	Asp	Tyr	Ala	Ile	Val	Asn	Asp	Gln	Val	Pro	Leu	Ala	Ala
				100				105					110		
Glu	Arg	Val	Lys	Cys	Val	Ile	Glu	Ala	Glu	His	Phe	Cys	Val	Asp	Arg
				115				120					125		
Val	Ile	Gly	His	Tyr	Gln	Glu	Met	Leu	Pro	Lys	Ser	Pro	Thr	Thr	Arg
				130				135					140		

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

Met	Ser	Arg	Leu	Leu	Val	Ile	Gly	Cys	Gly	Gly	Val	Ala	Gln	Val	Ala
1					5				10				15		
Ile	Ser	Lys	Ile	Cys	Gln	Asp	Ser	Glu	Thr	Phe	Thr	Glu	Ile	Met	Ile
					20				25				30		
Ala	Ser	Arg	Thr	Lys	Ser	Lys	Cys	Asp	Asp	Leu	Lys	Ala	Lys	Leu	Glu
					35				40				45		
Gly	Lys	Thr	Ser	Thr	Lys	Ile	Glu	Thr	Ala	Ala	Leu	Asp	Ala	Asp	Lys
					50				55				60		
Val	Glu	Glu	Val	Ile	Ala	Leu	Ile	Glu	Ser	Leu	Gln	Thr	Ser	Lys	Leu
				65				70					75		80
Phe															

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

Met His Glu Ser Phe His Val Asp Asp Pro Thr Leu Tyr Ser Arg Glu
1 5 10 15
Trp Phe Ser Trp Ala Asn Met Met Phe Cys Glu Leu Val Leu Asp Tyr
20 25 30
Leu Asp Ile Arg
35

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

Met Arg Phe Tyr Phe Met Glu Asn Val Val Val His Ile Ile Ser His
1 5 10 15
Ser His Trp Asp Arg Glu Trp Tyr Leu Pro Phe Glu Ser His Arg Met
20 25 30
Gln Leu Val Glu Leu Phe Asp Asn Leu Phe Asp Leu Phe Glu Asn Asp
35 40 45
Pro Glu Phe Lys Ser Phe His Leu Asp Gly Gln Thr Ile Val Leu Asp
50 55 60
Asp
65

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

Met Leu Leu Tyr Ile Leu Ser His Ile Ala Thr Gly Ile Val Ser Gly
1 5 10 15
Thr Cys Leu Leu Lys Ala Ile Val Cys Asn Trp Trp Asn Cys Leu Thr
20 25 30
Ile Ser Leu Ile Ser Leu Lys Met Thr Leu Ser Ser Arg Val Ser Thr
35 40 45
Trp Met Asp Lys Leu Leu Ser Leu Thr Thr Asn Leu Gln Ile Arg Pro
50 55 60
Glu Asn Arg Asp Lys Val Gln Arg Tyr Ile Asp Glu Gly Lys Leu Lys
65 70 75 80
Ile Gly Pro Phe Tyr Ile Leu Gln Asp Asp Tyr Leu Ile Ser Ser Glu
85 90 95
Ala Asn Val Arg Asn Thr Leu Ile Gly Gln Gln Glu Ala Ala Lys Trp
100 105 110
Gly Lys Ser Thr Gln Ile Gly Tyr Phe Pro Asp Thr Phe Gly Asn Met
115 120 125
Gly Gln Ala Pro Gln Ile Leu Gln Lys Ser Gly Ile His Val Ala Ala
130 135 140
Phe Gly Arg Gly Val Lys Pro Ile Gly Phe Asp Asn Gln Val Leu Glu
145 150 155 160
Asp Glu Gln Phe Thr Ser Gln Phe Ser Glu Met Tyr Trp Gln Gly Val
165 170 175
Asp Gly Ser Arg Val Leu Gly Ile Leu Phe Ala Asn Trp Tyr Ser Asn
180 185 190
Gly Asn Glu Ile Pro Val Asp Lys Asp Glu Ala Leu Thr Phe Trp Lys
195 200 205
Gln Lys Leu Ser Asp Val Arg Cys Leu Arg Phe Asp Gln Pro Met Val
210 215 220
Asp Asp Glu Thr Ala Val Asn Thr Ser Leu Ser Gln Lys Lys Ser Glu
225 230 235 240
Arg Ser His Ser Val Trp Gln Met Asn Ser Ser Arg Met
245 250

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

Met	Thr	Ile	Val	Gly	Cys	Arg	Ile	Asp	Gly	Arg	Leu	Ile	His	Gly	Gln
1							5			10					15
Val	Ala	Asn	Leu	Trp	Ala	Gly	Lys	Leu	Asn	Val	Ser	Arg	Ile	Met	Val
										20			25		30
Val	Asp	Asp	Glu	Val	Val	Asn	Asn	Asp	Ile	Glu	Lys	Ser	Gly	Leu	Lys
						35			40				45		
Leu	Ala	Thr	Pro	Pro	Gly	Val	Lys	Leu	Ser	Ile	Leu	Pro	Val	Glu	Lys
							50			55			60		
Ala	Ala	Ala	Asn	Ile	Leu	Ala	Gly	Lys	Tyr	Asp	Ser	Gln	Arg	Leu	Phe
						65			70			75			80
Ile	Val	Ala	Arg	Lys	Pro	Asp	Arg	Phe	Pro	Trp	Phe	Gly	Arg	Ser	Arg
						85			90				95		
Cys	Thr	Thr													

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

Met	Ile	Gln	His	Pro	Arg	Ile	Gly	Ile	Arg	Pro	Thr	Ile	Asp	Gly	Arg
1								5			10				15
Arg	Gln	Gly	Val	Arg	Glu	Ser	Leu	Glu	Val	Gln	Thr	Met	Asn	Met	Ala
									20		25			30	

Lys Ser Val Ala Asp Leu Ile Ser Ser Thr Leu Lys Tyr Pro Asp Gly
 35 40 45
 Glu Pro Val Glu Cys Val Ile Ser Pro Ser Thr Ile Gly Arg Val Pro
 50 55 60
 Glu Ala Ala Ala Ser His Glu Leu Phe Lys Lys Ser Asn Val Cys Ala
 65 70 75 80
 Thr Ile Thr Val Thr Pro Cys Trp Cys Tyr Gly Ser Glu Thr Met Asp
 85 90 95
 Met Ser Pro Asp Ile Pro His Ala Ile Trp Gly Phe Asn Gly Thr Glu
 100 105 110
 Arg Pro Gly Ala Val Tyr Leu Ala Ala Val Leu Ala Ser His Ala Gln
 115 120 125
 Lys Gly Ile Pro Ala Phe Gly Ile Tyr Gly Arg Asp Val Gln Glu Ala
 130 135 140
 Asn Asp Thr Asp Ile Pro Glu Asp Val Lys Glu Asn Phe
 145 150 155

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

Met Leu Leu Ser Thr Lys Gly Ile Glu Glu Gln Glu Ile Ala Arg Pro
 1 5 10 15
 Thr Leu Glu Arg Leu Phe Ser Met Arg Glu Asn Tyr Lys Val Thr Gly
 20 25 30
 Arg His Pro Gly Tyr Arg Lys Tyr Asn Gly Asp Gly Ser Met Lys Glu
 35 40 45
 Thr Glu Lys
 50

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

Met Leu Thr Leu Thr Pro Asp Val Ile Tyr Gln Glu Pro Asp Ile Leu
1 5 10 15
Tyr Gln His Glu Asp Phe Ser Leu Val Lys Ile Arg Gln Ile Arg Phe
20 25 30
Cys

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

Met Ser Ser Val Val Gly Leu Met Gly Asn Ile Gly Gln Ala Asn Tyr
1 5 10 15
Ala Ala Ser Lys Ala Gly Leu Ile Gly Phe Thr Lys Ser Val Ala Arg
20 25 30
Glu Val Ala Ser Arg Asn Ile Arg Val Asn Val Ile Ala Pro Gly Asn
35 40 45
Asp

(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

Met Lys Leu Glu His Lys Asn Ile Phe Ile Thr Gly Ser Ser Arg Gly
1 5 10 15
Ile Gly Leu Ala Ile Ala His Lys Phe Ala Gln Ala Gly Ala Asn Ile
20 25 30
Val Leu Asn Ser Arg Gly Ala Ile Ser Glu Glu Leu Leu Ala Glu Phe
35 40 45
Ser Asn Tyr Gly Ile Lys Val Val Pro Ile Ser Gly Asp Val Ser Asp
50 55 60
Phe Ala Asp Ala Lys Arg Met Ile Asp Gln Ala Ile Ala Glu Leu Gly
65 70 75 80
Ser Val Asp Val Leu Val Asn Asn Ala Gly Ile Thr Gln Asp Thr Leu
85 90 95
Met Leu Lys Met Thr Glu Ala Asp Phe Glu Lys Val Leu Lys Val Asn
100 105 110
Leu Thr Gly Ala Phe Asn Met Thr Gln Ser Val Phe Gly Asn Arg
115 120 125

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

Met Glu Ser Met Pro Arg Ile Gly Leu Leu Val Thr Val Glu Asn Arg
1 5 10 15
Asp Thr Glu Thr Ile Phe Asn Ala Ala Gly Leu Asp Phe Asp Val Leu
20 25 30
Lys Ala Ser Ala Ile Ala Tyr Ile Asn Ala Asn Thr Phe Val Gln Lys
35 40 45
Glu Asn Ala Gly Glu Met Gly Arg Ser Val Ser Tyr His Asp Met Arg
50 55 60
Ser Val
65

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

Met Arg Gln Gly Gln Gly Ser Val Glu Ala Ile Phe Asn Ala Ile Asp
1 5 10 15
Lys Phe Phe Asn Gln Ser Val Arg Leu Val Ser Tyr Thr Ile Asn Ala
20 25 30
Val Thr Asp Gly Ile Asp Ala Gln Asp Arg Val Val Gly His Cys
35 40 45

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

Met Val Glu Asn Pro Glu Gly Phe His Phe Asp Asp Leu Gln Leu Gln
1 5 10 15
Thr His Ala Asp Asn Asp Ile Glu Ala Leu Val Ser Leu Ala Asn Met
20 25 30
Asp Gly Glu Lys Val Glu Phe Asn Ala Thr Gly Thr Gly Phe Arg
35 40 45

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

Met Asn Phe Gln Leu Ala Lys Tyr Ser Leu Leu Lys Lys Phe Ser Glu
1 5 10 15
Asn Ile Gly Phe Thr Thr Pro Glu Glu Cys Gly Ala Ile Phe Gln Tyr
20 25 30
Leu Ile Glu Asn Val Gln Thr Asp Arg Gln Ile Ile Tyr Ser Pro Pro
35 40 45
Cys His Asp Glu Leu Arg Met Ala Val Ala Asn Ser Leu Ala Ala Val
50 55 60
Lys Asn Gly Ala Gly Leu Phe Glu Glu Thr Ile His Gly Ile Arg Glu
65 70 75 80
Arg Ala Glu Asn Ala Ala Leu Glu Glu Ile Ala Val Ala Leu Asn Ile
85 90 95
Arg Gln Asp Tyr Tyr Gln Val Glu Thr Ser Ile Val Leu Asn Glu Thr
100 105 110
Ile Asn Thr Ser Glu Met Val Ser Arg Phe Ser Gly Ile Pro Val Pro
115 120 125
Lys Asn Lys Ala Val Val Gly Gly Asn Thr Phe Ser His Glu Ser Gly
130 135 140
Ile His Gln Asp Gly Val Leu Lys Asn Pro Leu Thr Tyr Glu Ile Ile
145 150 155 160
Thr Pro Glu Leu Val Gly Val Lys Ile Pro Leu Gly Lys Leu Ser Gly
165 170 175
Arg His Ala Phe Val Glu Lys Leu Arg Glu Leu Ala Leu Asp Phe Thr
180 185 190
Glu Glu Asp Ile Lys Pro Phe Phe Ala Lys Phe Lys Ala Leu Ala Asp
195 200 205
Lys Lys
210

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

Met Ser Gln Gln Val Lys Asn Ala His Asn Leu Tyr Ile His Ala Ile
1 5 10 15
Gln Asp Gly Arg Val Ala Glu Ala Gln Ala Gln Ser Val Gly Asp Thr
20 25 30
Tyr Ile Gln His Ser Thr Gly Val Pro Asp Gly Lys Glu Gly Phe Ala
35 40 45
Ala Phe Phe Ala Asp Phe Phe Glu Arg His Pro Glu Arg Gln Ile Lys
50 55 60
Ile Val Arg Thr Ile Glu Asp Gly Asn Leu Val Phe Val His Val Pro
65 70 75 80
Ser Ile Ser Glu Trp Trp Arg Ser Ser Met Gly Asp Asp Gly Tyr Phe
85 90 95
Pro Cys Gly

(2) INFORMATION FOR SEQ ID NO:329:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 122 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

Met Glu Met Gln Thr Ser Ala Gln Leu Leu Thr Asn Lys Ile Phe Leu
1 5 10 15
Lys Asn Pro Leu Lys Ala Leu Val Glu Glu Lys Tyr Gly Ile Glu Tyr
20 25 30
Glu Glu Phe Thr Asn Pro Trp His Ala Ala Ile Ser Ser Phe Val Ala
35 40 45
Phe Phe Leu Arg Ser Leu Pro Pro Met Leu Ser Val Thr Ile Phe Pro
50 55 60
Ser Glu Tyr Arg Ile Pro Ala Thr Val Leu Ile Val Gly Val Ala Leu
65 70 75 80
Leu Leu Thr Gly Tyr Thr Ser Ala Arg Leu Gly Lys Asp Pro Thr Arg
85 90 95
Thr Ala Met Ile Arg Asn Leu Ala Ile Gly Leu Leu Thr Met Gly Val
100 105 110
Thr Phe Leu Leu Glu Gln Leu Phe Ser Ile
115 120

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

Met	Ala	Phe	Phe	Leu	Cys	Pro	His	Phe	Arg	Ser	Asn	His	Trp	Lys	Ile
1								5				10			15
Leu	Thr	Val	Ser	Asp	Thr	Met	Glu	Glu	Lys	Arg	Leu	Glu	Tyr	Pro	Met
						20					25				30
Val	Thr	Phe	Leu	Gly	Asn	Pro	Val	Ser	Phe	Thr	Gly	Lys	Gln	Leu	Gln
							35			40				45	
Val	Gly	Asp	Lys	Ala	Leu	Asp	Phe	Ser	Leu	Thr	Thr	Thr	Asp	Leu	Ser
						50			55			60			
Lys	Lys	Ser	Leu	Ala	Asp	Phe	Asp	Gly	Lys	Lys	Val	Leu	Ser	Val	
						65			70		75			80	
Val	Pro	Ser	Ile	Asp	Thr	Gly	Ile	Cys	Ser	Thr	Gln	Thr	Arg	Arg	Phe
						85			90			95			
Asn	Glu	Glu	Leu	Ala	Gly	Leu	Asp	Asn	Thr	Val	Val	Leu	Thr	Val	Ser
						100			105			110			
Met	Asp	Leu	Pro	Phe	Ala	Gln	Lys	Arg	Trp	Cys	Gly	Ala	Glu	Gly	Leu
						115			120			125			
Asp	Asn	Ala	Ile	Met	Leu	Ser	Asp	Tyr	Phe	Asp	His	Ser	Phe	Gly	Arg
						130			135			140			
Asp	Tyr	Ala	Leu	Leu	Ile	Asn	Glu	Trp	His	Leu	Leu	Ala	Arg	Ala	Val
						145			150			155			160
Phe	Val	Leu	Asp	Thr	Asp	Asn	Thr	Ile	Arg	Tyr	Val	Glu	Tyr	Val	Asp
						165			170			175			
Asn	Ile	Asn	Ser	Glu	Pro	Asn	Phe	Glu	Ala	Ala	Ile	Ala	Ala	Lys	
						180			185			190			
Ala	Leu														

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

Met Gly Tyr Arg Pro Ser Thr Ala Asn Ala Ile Ile His Gln Val Arg
1 5 10 15
Glu Leu Leu Val Ser Arg Gly Tyr Thr Phe Tyr Asn Arg Lys Arg Leu
20 25 30
Met Val Val Pro Lys Ser Val Val Lys Glu Leu Leu Gly Met Glu Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

Met Gln Ala Val Glu His Phe Ile Lys Gln Phe Val Pro Glu His Tyr
1 5 10 15
Asp Leu Phe Leu Asp Leu Ser Arg Glu Thr Lys Thr Phe Ser Gly Lys
20 25 30
Val Thr Ile Thr Gly Gln Ala Gln Ser Asp Arg Ile Ser Leu His Gln
35 40 45
Lys Asp Leu Glu Ile Thr Ser Val Glu Val Ala Gly Gln Ala Arg Pro
50 55 60
Phe Thr Val Asp His Asp Asn Glu Ala Leu His Ile Glu Leu Ala Glu
65 70 75 80
Ala Gly Gln Val Glu Leu Val Leu Ala Phe Ser Gly Lys Ile Thr Asp
85 90 95
Asn Met Thr Gly Ile Tyr Pro Ser Tyr Tyr Thr Val Asp Gly Val Lys
100 105 110
Lys Glu Val Leu Ser Thr Gln Phe Glu Ser His Phe Ala Arg Glu Ala
115 120 125

Phe Pro Cys Val Asp Glu Pro Glu Ala Lys Ala Thr Phe Asp Leu Ser
130 135 140
Leu Arg Phe Asp Gln Ala Glu Gly Glu Leu Ala Leu Ser Asn Met Pro
145 150 155 160
Glu Ile Asp Val Glu Asn Arg Lys Glu Thr Gly Ile Trp Lys Phe Glu
165 170 175
Thr Thr Pro Arg Met Ser Ser Tyr Leu Leu Ala Phe Val Ala Gly Asp
180 185 190
Leu Gln Gly Val Thr Ala Lys Thr Lys Asn Gly Thr Leu Val Gly Cys
195 200 205
Leu Leu Asn Gln Ser Thr Ser Thr Phe Lys Ser
210 215

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

Met Ser Gln Glu Phe Leu Ala Arg Ile Leu Glu Gln Lys Ala Arg Glu
1 5 10 15
Val Glu Gln Met Lys Leu Glu Gln Ile Gln Pro Leu Arg Gln Thr Tyr
20 25 30
Arg Leu Ala Glu Phe Leu Lys Asn His Gln Asp Arg Leu Gln Val Ile
35 40 45
Ala Glu Val Lys Lys Ala Ser Pro Ser Phe Gly Glu Ile Ser Ile Ser
50 55 60
Met Trp Ile Leu Cys Asn Arg Pro Arg Leu Met Lys Lys Thr Glu Gln
65 70 75 80

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

Met	Ser	Ser	Phe	Thr	Pro	Glu	Asp	Leu	Gly	Met	Glu	Gly	Tyr	Ala	Met
1					5					10					15
Glu	Asp	Ile	Arg	Gly	Gly	Asn	Ala	Gln	Glu	Asn	Ala	Glu	Ile	Leu	Leu
					20				25					30	
Ser	Val	Leu	Lys	Asn	Glu	Ala	Ser	Pro	Phe	Leu	Glu	Thr	Thr	Val	Leu
					35				40					45	
Asn	Ala	Gly	Leu	Gly	Phe	Tyr	Ala	Asn	Gly	Lys	Ile	Asp	Ser	Ile	Lys
					50				55					60	
Glu	Gly	Val	Ala	Leu	Ala	Arg	Gln	Val	Ile	Ala	Arg	Gly	Lys	Ala	Leu
					65				70			75		80	
Glu	Lys	Leu	Arg	Leu	Leu	Gln	Glu	Tyr	Gln	Lys					
					85				90						

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

Met	Ile	Tyr	Thr	Val	Thr	Leu	Asn	Pro	Ser	Ile	Asp	Tyr	Ile	Val	Arg
1						5				10					15
Leu	Asp	Gln	Val	Lys	Val	Gly	Ser	Val	Asn	Arg	Met	Asp	Ser	Asp	Asp
						20				25				30	
Lys	Phe	Ala	Gly	Gly	Lys	Gly	Ile	Asn	Val	Ser	Arg	Val	Leu	Lys	Arg
						35				40				45	
Leu	Asn	Ile	Ser	Asn	Thr	Ala	Thr	Gly	Phe	Ile	Gly	Gly	Phe	Thr	Gly
						50				55				60	
Lys	Phe	Xaa	Xaa	Asp	Thr	Leu	Ala	Glu	Glu	Ile	Glu	Xaa	Arg	Phe	
						65				70				80	
Val	Gln	Val	Ala	Glu	Asp	Thr	Arg	Ile	Asn	Val	Lys	Ile	Xaa	Ala	Asp
						85				90				95	
Gln	Glu	Thr	Glu	Ile	Asn	Gly	Thr	Gly	Pro	Thr	Val	Glu	Pro	Val	Lys
						100				105				110	

Leu Glu Glu Leu Lys Ala Ile Leu Ser Ser Leu Thr Ala Glu Asp Thr
115 120 125
Val Val Phe Ala Gly Ser Ser Ala Lys Asn Leu Gly Asn Val Ile Tyr
130 135 140
Lys Gly Phe Asn Leu Leu Asp Ala Pro Asp Trp Cys Ala Ser Gly Leu
145 150 155 160

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

Met Met Gln Val Tyr Phe Asp Gln Gly Ile Tyr Asn Lys Lys Ala Val
1 5 10 15
Phe Glu Val Tyr Phe Arg Gln Gln Pro Phe Lys Asn Gly Tyr Ala Val
20 25 30
Phe Ala Gly Leu Glu Arg Ile Val Asn Tyr Leu Glu Asp Leu Arg Phe
35 40 45
Ser Asp Ser Asp Ile Ala Tyr Leu Glu Ser Leu Gly Tyr His Gly Ala
50 55 60
Phe Leu Asp Tyr Leu Arg Asn Phe Lys Leu Glu Leu Thr Val Arg Ser
65 70 75 80
Ala Gln Glu Gly Asp Leu Val Phe Ala Asn Glu Pro Ile Val Gln Val
85 90 95
Glu Gly Pro Leu Ala Gln Cys Gln Leu Val Glu Thr Ala Leu Leu Asn
100 105 110
Ile Val Asn Tyr Gln Thr Leu Val Ala Thr Lys Ala Ala Pro Tyr Pro
115 120 125
Phe Gly Tyr Arg Lys
130

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

Met	Lys	Ile	Ile	Ile	Gln	Arg	Val	Lys	Lys	Ala	Gln	Val	Ser	Ile	Glu	
1								5				10			15	
Gly	Gln	Ile	Ile	Gln	Gly	Lys	Ile	Asn	Gln	Gly	Leu	Leu	Leu	Leu	Val	Gly
							20				25			30		
Val	Gly	Pro	Glu	Asp	Gln	Glu	Glu	Asp	Leu	Asp	Tyr	Ala	Val	Arg	Lys	
							35				40			45		
Leu	Val	Asn	Met	Arg	Ile	Phe	Ser	Asp	Val	Glu	Gly	Lys	Met	Asn	Leu	
			50					55				60				
Ser	Val	Lys	Asp	Ile	Glu	Gly	Glu	Ile	Leu	Ser	Ile	Leu	Ser	Leu	Pro	
			65				70				75			80		
Leu	Cys	Gly	Tyr													

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

Met	Ile	Lys	Gly	Thr	Ile	Lys	Thr	Val	Ser	Ile	Met	Ala	Ala	Thr	Ser	
1								5				10			15	
Gly	Phe	Leu	Leu	Tyr	Asn	Glu	Val	Phe	Phe	Leu	Thr	Asn	Gly	Ala	Ala	
							20				25			30		
Gly	Thr	Lys	Ser	Ile	Ser	Phe	Val	Ile	Arg	Glu	Leu	Ala	Val	Ala	Ser	
							35				40			45		
Ser	Arg	Thr	Gln	Tyr	Ala	Arg	Ala	Asn	Thr	Ile	Gly	Val	Ile	Gln	Ile	
							50				55			60		
Leu	Gly	Gly	Met	Leu	Ile	Ile	Val	Cys	Ile	Asn	Ile	Leu	Phe	Arg	Glu	
			65				70				75			80		
Arg	Lys	Arg	Leu	Lys	Gly	Gly	Lys									
							85									

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

Met Gly Phe Gly Ile Pro Ala Ala Ile Gly Ala Lys Ile Ala Asn Pro
1 5 10 15
Asp Lys Glu Val Val Leu Phe Val Gly Asp Gly Gly Phe Gln Met Thr
20 25 30
Asn Gln Glu Leu Ala Ile Leu Asn Ile Tyr Lys Val Pro Ile Lys Val
35 40 45
Val Met Leu Asn Asn His Ser Leu Gly Met Val Arg Gln Trp Gln Glu
50 55 60
Ser Phe Tyr Glu Gly Arg Thr Ser Glu Ser Val Phe Asp Thr Leu Pro
65 70 75 80
Asp Phe Gln Leu Met Ala Gln Ala Tyr Gly Ile Lys Asn Tyr Lys Phe
85 90 95
Asp Asn Pro Glu Thr Leu Ala Gln Asp Leu Glu Ala Thr Thr Glu Asp
100 105 110
Val Pro Met Leu Ile Glu Val Asp Ile Ser Arg Lys Glu Gln Val Leu
115 120 125
Pro Met Val Pro Ala Gly Lys Ser Asn His Glu Met Leu Gly Val Lys
130 135 140
Phe His Ala
145

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

Met Trp Leu Pro Leu Asp Arg Asn Asn Lys Gly Gln Asn Ile Ala Gly
 1 5 10 15
 Ala Arg Gln Ala Ala Glu Gly Ile Phe Gly Val Asp Ala Ser Gln Leu
 20 25 30
 Thr Val Pro Gln Ala Ala Phe Leu Ala Gly Leu Pro Gln Ser Pro Ile
 35 40 45
 Thr Tyr Ser Pro Tyr Glu Asn Thr Gly Glu Leu Lys Asn
 50 55 60

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

Met Tyr Leu Gly Asp Leu Met Glu Lys Ala Glu Cys Gly Gln Phe Ser
 1 5 10 15
 Ile Leu Ser Phe Leu Leu Gln Glu Ser Gln Thr Thr Val Lys Ala Val
 20 25 30
 Met Glu Glu Thr Gly Phe Ser Lys Ala Thr Leu Thr Lys Tyr Val Thr
 35 40 45
 Leu Leu Asn Asp Lys Ala Leu Asp Ser Gly Leu Glu Leu Thr Ile His
 50 55 60
 Ser Glu Asp Glu Asn Leu Arg Leu Ser Ile Gly Ala Ala Thr Lys Gly
 65 70 75 80
 Arg Asp Ile Pro Glu Leu Val Phe Trp Ile Val Leu Leu Asn Thr Arg
 85 90 95
 Phe Trp Phe Ile Phe Ser Thr Thr Asn Ser Phe
 100 105

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

Met Lys Glu Ile Ile Glu Lys Leu Ala Lys Phe Glu Asn Leu Ser Gly
1 5 10 15
Val Glu Met Thr Asp Val Ile Glu Arg Ile Val Thr Gly Arg Val Thr
20 25 30
Glu Ala Gln Ile Ala Ser Leu Leu Ala Leu Lys Met Lys Gly Glu
35 40 45
Thr Pro Glu Glu Arg Thr Ala Ile Ala Gln Val Met Arg Gly His Ala
50 55 60
Gln His Ile Pro Thr Glu Ile His Asp Ala Met Asp Asn Cys Gly Thr
65 70 75 80
Gly Gly Asp Lys Ser Phe Ser Phe Asn Ile Ser Thr Thr Ala Ala Phe
85 90 95
Val Leu Ala Gly Gly Ile His Met Ala Lys His Gly Asn Arg Ser
100 105 110
Ile Ser Ser Lys Ser Gly Ser Ala Asp Ser Xaa Asn Leu Gly Asn Gln
115 120 125
Ser

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

Met Asn Val Gln Met Ser Ser Lys Thr Asn Ile Leu Arg Ala His Ala
1 5 10 15
Glu Met Gln Asn Ile Gln Arg Arg Ala Asn Glu Glu Arg Gln Asn Leu
20 25 30
Gln Arg Tyr Arg Ser Gln Asp Leu Ala Lys Ala Ile Leu Pro Ser Leu
35 40 45
Asp Asn Leu Glu Arg Ala Leu Ala Val Glu Gly Leu Thr Asp Asp Val
50 55 60

Lys Lys Gly Leu Gly Met Val Gln Glu Ser Leu Ile His Ala Leu Lys
65 70 75 80
Glu Glu Gly Ile Glu Glu Ile Ala Ala Asp Gly Glu Phe Asp His Asn
85 90 95
Tyr His Met Ala Ile Gln Thr Leu Pro Ala Asp Asp Asp His Pro Val
100 105 110
Asp Thr Ile Ala Gln Val Phe Gln Lys Gly Tyr Lys Leu His Asp Arg
115 120 125
Ile Leu Arg Pro Ala Met Val Val Val Tyr Asn
130 135

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

Met Ser Asn Lys Ser Tyr Ser Lys Phe Gln Glu Glu Val Ser Leu Lys
1 5 10 15
Tyr Gly Phe Ile Gly Leu Lys Leu Asp Lys Leu Ser Leu Thr Ala Glu
20 25 30
Val Ser Glu Glu Phe His Ser Glu Ile Leu Ser Gly Asn Phe Thr Leu
35 40 45
Tyr Asp Ile Ser Val
50

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

Met His Phe Asp Lys Ser Lys Phe Gly Ala Val Phe Ser Ala Pro Gly
 1 5 10 15
 Leu Tyr Glu Val Glu Val Ile Asn Asn Ala Ser Phe Gly Gln Asn Ala
 20 25 30
 Gln Tyr Glu Val Ile Gln Ser Arg Lys Leu Gly Thr Phe Ala Glu Leu
 35 40 45
 Ile Glu Met Ala Lys Ile Lys
 50 55

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

Met Ile Gln Ala Val Phe Glu Arg Ala Glu Asp Gly Glu Leu Arg Ser
 1 5 10 15
 Ala Glu Ile Thr Gly His Ala Glu Ser Gly Glu Tyr Gly Leu Asp Val
 20 25 30
 Val Cys Ala Ser Val Ser Thr Leu Ala Ile Asn Phe Ile Asn Ser Ile
 35 40 45
 Glu Lys Phe Ala Gly Tyr Glu Pro Ile Leu Glu Leu Asn Glu Asp Glu
 50 55 60
 Gly Gly Tyr Leu Met Val Glu Ile Pro Lys Asp Leu Pro Ser His Gln
 65 70 75 80
 Arg Glu Met Thr Gln Leu Phe Phe Glu Ser Phe Phe Leu Gly Met Ala
 85 90 95
 Asn Leu Ser Glu Asn Ser Ser Glu Phe Val Gln Thr Arg Val Ile Thr
 100 105 110
 Glu Asn

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

Met	Thr	Ala	Ile	Ser	Met	Lys	Trp	Leu	Asn	Asp	Tyr	Ile	Trp	Pro	Ala
1					5				10				15		
Glu	Ser	Glu	Phe	Thr	Pro	Asp	Met	Thr	Thr	Asn	Ala	Val	Lys	Glu	Ala
					20				25			30			
Leu	Thr	Glu	Met	Leu	Gln	Ser	Gly	Thr	Thr	Phe	Asn	Asp	Met	Tyr	
					35				40			45			
Asn	Pro	Asn	Gly	Val	Asp	Ile	Gln	Gln	Ile	Tyr	Gln	Val	Val	Lys	Thr
					50				55			60			
Ser	Lys	Met	Arg	Cys	Tyr	Phe	Ser	Pro	Thr	Leu	Phe	Ser	Ser	Glu	Thr
					65				70			75			80
Glu	Thr	Thr	Ala	Glu	Thr	Ile	Ser	Arg	Thr	Arg	Ser	Ile	Ile	Asp	Glu
					85				90			95			
Ile	Leu	Lys	Tyr	Lys	Asn	Pro	Lys	Phe	Gln	Gly	Leu	Trp			
					100				105						

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

Met	Val	Arg	Glu	Ser	Ala	Glu	Ser	Ala	Gly	Phe	Phe	Leu	Glu	Thr	His
1					5				10			15			
Met	Val	Gln	Gly	Glu	Trp	Asn	Thr	Cys	Val	Phe	Lys	Lys	Thr	Lys	Asp
					20				25			30			
Ile	Ser	Gly	Val	Ile	Gly	Gly									
					35										

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

Met Thr Val Asp Arg Glu Gly Phe Glu Ala Ala Met Lys Glu Gln Gln
1 5 10 15
Glu Arg Ala Arg Ala Ser Ala Val Lys Gly Gly Ser Met Gly Met Gln
20 25 30
Asn Gly Asn Ser Ser Lys His His Cys Arg Lys Cys Cys Leu Gln Leu Gln
35 40 45
Cys

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

Met Lys Ala Gln Leu Val Pro Ser Arg Ser Lys Tyr Leu Ile Asn Asp
1 5 10 15
Asn Thr Val Val Leu Phe Phe Gly Thr Arg Thr Asp Tyr Thr Arg Lys
20 25 30
Tyr Asp Leu Asp Leu Val Arg Glu Val Ala Gly Asp Gln Ile Ala Arg
35 40 45
Arg Val Val Leu Leu Ser Asp Gln Ala Phe Gly Leu Glu Asn Val Lys
50 55 60
Glu Val Ala Leu Gly Cys Gly Gly Val Leu Asn Asp Ile Tyr Arg Val
65 70 75 80
Phe Pro Tyr Ile Val Tyr Ala Gln Leu Phe Ala Leu Leu Thr Ser Leu
85 90 95
Lys Val Glu Asn Lys Pro Asp Thr Pro Ser Pro Thr Gly Thr Val Asn
100 105 110

Arg Val Val Gln Gly Val Ile Ile His Glu Tyr Gln Lys
 115 120 125

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

```

Met Ala Val Asn Asn Glu Ile Gly Ser Ile Gln Xaa Ile Glu Ala Ile
  1                5                10                15
Ser Glu Phe Leu Ala Asp Lys Pro Thr Ile Ser Phe His Val Asp Ala
  20                25                30
Val Gln Ala Leu Ala Lys Ile Pro Thr Glu Lys Tyr Leu Thr Glu Arg
  35                40                45
Val Asp Cys Ala Thr Phe Ser Ser His Lys Phe His Gly Val Arg Gly
  50                55                60
Val Gly Phe Val Tyr Ile Lys Ser Gly Lys Lys Ile Thr Pro Leu Leu
  65                70                75                80
Thr Gly Gly Gln Glu Arg Asp Tyr Arg Ser Thr Thr Glu Asn Val
  85                90                95
Ala Gly Ile Ala Ala Thr Ala Lys Ala Leu Arg Leu Ser Met Glu Lys
 100                105                110
Leu Asp Ile Phe Arg Ser Lys Thr Gly Gln Met Lys Ala Val Ile His
 115                120                125
Gln Ala Leu Leu Asn Tyr Pro Asp Ile Phe Val Phe Ser Asp Glu Glu
 130                135                140
Asp Phe Ala Pro His Ile Leu Thr Phe Gly Ile Lys Gly Val Arg Gly
 145                150                155                160
Glu Val Ile Val His Ala Phe Glu Asp Tyr Asp Ile Phe Ile Ser Thr
 165                170                175
Thr Ser Ala Cys Ser Ser Lys Ala Gly Lys Pro Ala Gly Thr Leu Ile
 180                185                190
Ala Met Gly Val Asp Lys Asp Lys Ala Lys Ser Ala Val Arg Leu Ser
 195                200                205
Leu Asp Leu Glu Asn Asp Met Ser Gln Val Glu Gln Phe Leu Thr Lys
 210                215                220

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Leu Lys Leu Ile Tyr Asn Gln Thr Arg Lys Val Arg
225 230 235

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

Met Leu Val Thr Gly Ala Ile Leu Gly Val Asn Val His Ile Phe Ser
1 5 10 15
Pro Lys Glu Leu Phe Pro Glu Lys Glu Ile Val Glu Leu Ala Glu Gly
20 25 30
Phe Ala Lys Glu Ser Gly Ala His Val Leu Ile Thr Glu Asp Ala Asp
35 40 45
Glu Ala Val Lys Asp Ala Asp Val Leu Tyr Thr Asp Val Trp Val Ser
50 55 60
Met Gly Glu Glu Asp Lys Phe Ala Glu Arg Val Ala Leu Leu Lys Pro
65 70 75 80
Tyr Gln Val Asn Met Asp Leu Val Lys Lys Ala Gly Asn Glu Asn Leu
85 90 95
Ile Phe Leu His Cys Leu Pro Ala Phe His Asp Thr His Thr Val Tyr
100 105 110
Gly Lys Asp Val Ala Glu Lys Phe Gly Val Glu Glu Met Glu Val Thr
115 120 125
Asp Glu Val Phe Arg Ser Lys Tyr Ala Arg His Phe Asp Gln Ala Glu
130 135 140
Asn Arg Met His Thr Ile Lys Ala Val Met Ala Ala Thr Leu Gly Asn
145 150 155 160
Leu Tyr Ile Pro Lys Val
165

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

Met	Arg	Leu	Glu	Gln	Asp	Cys	Pro	Val	Phe	Leu	Lys	Ile	Lys	Glu	Lys
1															15
Asp	Met	Ala	Ser	Lys	Met	Leu	His	Thr	Cys	Leu	Arg	Val	Glu	Asn	Leu
					20					25					30
Glu	Lys	Ser	Ile	Ala	Phe	Tyr	Gln	Asp	Ala	Phe	Gly	Phe	Lys	Glu	Leu
					35				40						45
Arg	Arg	Arg	Asp	Phe	Pro	Asp	His	Ala	Phe	Thr	Ile	Val	Tyr	Leu	Gly
					50				55						60
Leu	Glu	Gly	Asp	Asp	Tyr	Glu	Leu	Glu	Leu	Thr	Tyr	Asn	Tyr	Asp	His
					65			70			75				80
Gly	Pro	Tyr	Val	Val	Gly	Asp	Gly	Phe	Ala	His	Ile	Ala	Leu	Ser	Thr
					85				90						95
Pro	Asp	Leu	Glu	Ala	Leu	His	Gln	Glu	His	Ser	Thr	Lys	Gly	Tyr	Glu
					100				105						110
Val	Thr	Glu	Pro	Asn	Gly	Leu	Pro	Gly	Thr	Ala	Pro	Asn	Tyr	Tyr	Phe
					115				120						125
Val	Lys	Asp	Pro	Asp	Gly	Tyr	Lys	Val	Glu	Val	Ile	Arg	Glu	Lys	
					130				135						140

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

Met	Asp	His	Thr	Ile	Phe	Cys	Val	Gly	Tyr	Arg	Val	Met	Gln	Lys	Asp
1															15
Leu	Glu	Gly	Thr	Leu	Asp	Ala	Glu	Lys	Leu	Lys	Ala	Ala	Gly	Val	Pro
					20				25						30
Phe	Gly	Pro	Leu	Phe	Gly	Lys	Ile	Lys	Asn	Gly	Gln	Asp	Leu	Val	Leu
					35				40						45

Glu Asp Gly Thr Glu Ile Lys Ala Ala Asp Tyr Ile Ser Ala Pro Arg
50 55 60
Pro Gly Lys Ile Ile Thr Ile Leu Gly Asp Thr Arg Lys Thr Asp Ala
65 70 75 80
Ser Val Arg Leu Ala Val Asn Ala Asp Val Leu Val His Glu Ser Thr
85 90 95
Tyr Gly Lys Gly Asp Glu Lys Ile Ala Arg Asn His Gly His Ser Thr
100 105 110
Asn Met Gln Ala Ala Gln Val Ala Val Glu Ala Gly Ala Lys Arg Leu
115 120 125
Leu Leu Asn His Ile Ser Ala Arg Phe Leu Ser Lys Asp Ile Ser Lys
130 135 140
Leu Lys Lys Asp Ala Ala Thr Ile Phe Glu Asn Val His Val Val Lys
145 150 155 160
Asp Leu Glu Lys Met Glu Ile Tyr Gln Ser Gln Lys Gly
165 170

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

Met Ile Gln Pro Ala Ser Leu Glu Glu Leu Ala Ser Leu Val Glu Lys
1 5 10 15
Ala Gly Lys Lys Val Phe Leu Phe Val Ala Asp Trp Cys Gly Asp Cys
20 25 30
Arg Tyr Ile Tyr Pro Ala Leu Pro Glu Ile Glu Glu Thr Asn Pro Glu
35 40 45
Phe Thr Phe Ile Arg Met Asp Arg Asp Gln Tyr Met Asp Leu Ala Lys
50 55 60
Leu Trp Asp Val Tyr Gly Ile Pro Ser Leu Val Val Leu Glu Lys Asp
65 70 75 80
Lys Glu Ile Gly Arg Phe Val Asn Arg Asp Arg Lys Ser Lys Glu Gln
85 90 95
Ile Asn Asp Phe Leu Ala Gly Leu Lys
100 105

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

Met Arg Leu Gly Leu Leu Gln Val Leu Arg Leu Pro Lys Ala Phe Gln
1 5 10 15
Leu Ile Phe Ile Gln Asp Lys Gly His Gly Asp Val Ser Ser Phe Thr
20 25 30
Ala Ser Cys Val Thr Gly Pro Trp Ala Phe Lys Leu Val Gly Lys Gln
35 40 45
Gly Asn Ile His
50

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

Met Lys Thr Arg Lys Ile Pro Leu Arg Lys Ser Val Val Ser Asn Glu
1 5 10 15
Val Ile Asp Lys Arg Asp Leu Leu Arg Ile Val Lys Asn Lys Glu Gly
20 25 30
Gln Val Phe Ile Asp Pro Thr Gly Lys Ala Asn Gly Arg Gly Ala Tyr
35 40 45
Ile Lys Leu Asp Asn Ala Glu Ala Leu Glu Ala Lys Lys Lys Val
50 55 60
Phe Asn Arg Ser Phe Ser Met Glu Val Glu Glu Ser Phe Tyr Asp Glu
65 70 75 80

Leu Ile Ala Tyr Val Asp His Lys Val Lys Arg Arg Glu Leu Gly Leu
85 90 95
Glu

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

Met Arg Val Ala Tyr Phe Lys Val His His Pro Ile Tyr Tyr Tyr Cys
1 5 10 15
Ala Tyr Phe Ser Ile Arg Ala Lys Ala Phe Asp Ile Lys Thr Met Gly
20 25 30
Ala Gly Leu Glu Val Ile Lys Arg Arg Met Glu Glu Ile Ser Glu Lys
35 40 45
Arg Lys Asn Asn Glu Ala Ser Asn Val Glu Ile Asp Leu Tyr Thr Thr
50 55 60
Leu Glu Ile Val Asn Glu Met Trp Glu Arg Gly Phe Lys Phe Gly Lys
65 70 75 80
Leu Asp Leu Tyr Cys Ser Gln Thr Thr Glu Phe Leu Ile Asp Gly Asp
85 90 95
Thr Leu Ile Pro Pro Phe Val Ala Met Asp Gly Leu Gly Glu Asn Val
100 105 110
Ala Lys Gln Leu Val Arg Ala Arg Glu Glu Gly Glu Phe Leu Ser Lys
115 120 125
Thr Glu Leu Arg Lys Arg Gly Gly Leu Ser Ser Thr Leu Val Glu Lys
130 135 140
Met Asp Glu Met Gly Ile Leu Gly Asn Met Pro Glu Ile Thr Ser
145 150 155

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

Met Ser Ser Lys Ile Ser Ile Gly Gln Leu Ile Thr Phe Asn Thr Leu
1 5 10 15
Leu Ser Tyr Phe Thr Thr Pro Met Glu Asn Ile Ile Asn Leu Gln Thr
20 25 30
Lys Leu Gln Ser Ala Lys Val Ala Asn Asn Arg Leu Asn Glu Val Tyr
35 40 45
Leu Val Glu Ser Glu Phe Gln Val Gln Glu Asn Pro Val His Ser His
50 55 60
Phe Leu Met Gly Asp Ile Glu Phe Asp Asp Leu Ser Tyr Lys Tyr Gly
65 70 75 80
Phe Gly Arg Asp Thr Leu Thr Asp Ile Asn Leu Thr Ile Lys Gln Gly
85 90 95
Asp Lys Val Ser Leu Val Gly Val Ser Gly Ser Gly Lys Thr Thr Leu
100 105 110
Ala Lys Met Ile Val Asn Phe Phe Glu Pro Tyr Lys Gly His Ile Ser
115 120 125
Ile Asn His Gln Asp Ile Lys Asn Ile Asp Lys Lys Ser Leu Ala Pro
130 135 140
Ser Tyr
145

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

Met Arg Gln Ala Pro Ala Leu Ala Gln Ala Asn Ile Glu Arg Val Val
1 5 10 15
Val His Lys Ile Ser Lys Val Trp Glu Phe His Phe Arg Ile Phe
20 25 30

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

Met Gln Thr Gly Trp Gln Tyr Leu Gly Asn Lys Trp Tyr Tyr Leu Arg
1 5 10 15
Ser Ser Gly Ala Met Ala Thr Gly Trp Tyr Gln Glu Gly Thr Thr Trp
20 25 30
Tyr Tyr Leu Asp Gln Pro Asn Gly Asp Met Lys Thr Gly Trp Gln Asn
35 40 45
Leu Gly Asn Lys Trp Tyr Tyr Leu Arg Ser Ser Gly Ala Met Ala Thr
50 55 60
Gly Trp Tyr Gln Glu Gly Thr Thr Trp Tyr Tyr Leu Asp Gln Pro Asn
65 70 75 80
Gly Asp Met Lys Thr Gly Trp Gln Asn Leu Gly Asn Lys Trp Tyr Tyr
85 90 95
Leu Arg Ser Ser Gly Ala Met Ala Thr Gly Trp Tyr Gln Asp Gly Ser
100 105 110
Thr Trp Tyr Tyr Leu Asn Ala Val Met Glu Ile
115 120

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

Met Lys Trp Gly Ser Arg Ile Leu Leu Gly Leu Thr Pro Lys Ser Leu
1 5 10 15

Arg Tyr Arg Ile Trp Lys Lys Ala Glu Lys Glu Met Thr Lys Tyr Asp
20 25 30
Leu Ala Asp Cys Asp Gly Ile Thr Glu Leu Cys Ser Gly Pro Gly Tyr
35 40 45
Met Arg Asn Lys Tyr Pro Ile Thr Ser Phe Glu Asp Asn Leu Phe Leu
50 55 60
Pro Phe Glu Gly Thr Glu Met Pro Ile Pro Ile Gly Tyr Asp Val Tyr
65 70 75 80
Leu Arg Thr Ala Phe Gly Asp Tyr Met Thr Pro Pro Pro Ala Asp Lys
85 90 95
Gln Val Pro His Gln Asp Ala Val Ile Ala Asp Met Asp Lys Ser Tyr
100 105 110
Thr Glu Tyr Lys Gly Glu Tyr Gly Gly
115 120

(2) INFORMATION FOR SEQ ID NO:363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

Met Phe Pro Asp Ser Ile Asp Thr Met His Gln Ala Asn Glu Phe Ile
1 5 10 15
Ala Leu Asp Asp Leu Phe Arg Ala Ala Ala Ile Tyr Ala Glu Ala Ile
20 25 30
Tyr Glu Leu Ile Lys
35

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

Met Asp Glu Leu Gln Lys Arg Asn Leu Leu Gly Phe Val Phe Gln Asp
1 5 10 15
Phe Gln Leu Phe Pro His Leu Ser Val Leu Glu Asn Leu Thr Leu Ser
20 25 30
Pro Val Lys Thr Met Gly Met Lys Gln Glu Glu Ala Glu Lys Lys Ala
35 40 45
Ser Gly Leu Leu Glu Gln Leu Gly Leu Gly Gly His Ala Glu Ser Tyr
50 55 60
Pro Phe Ser Leu Ser Gly Gly Gln Lys Gln Arg Val Ala Leu Ala Arg
65 70 75 80
Ala Met Met Ile Asp Pro Glu Ile Ile Gly Tyr Asp Glu Pro Thr Ser
85 90 95
Ala Leu Asp Pro Glu Leu Arg Leu Glu Val Glu Lys Leu Ile Leu Gln
100 105 110
Asn Arg Glu Leu Gly Met Thr His Ile Val Val Thr His Asp Leu Gln
115 120 125
Phe Gly
130

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

Met Tyr Gly Ala Asn Ser Glu Arg Leu Lys Glu Ser Leu Arg Ile Ser
1 5 10 15
Leu Ser Pro Gln Asn Thr Val Glu Asp Leu Gln Thr Leu Ala Lys Thr
20 25 30
Leu Lys Glu Ile Ile Gly Gly
35

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

Met Ile Ala Arg Ser Tyr Gln Glu Met Asp Asp Leu Asp Thr Ala Tyr
1 5 10 15
Glu His Tyr Gln Glu Leu Thr Gly Asp Leu Lys Asp Asn Pro Glu Phe
20 25 30
Leu Glu His Tyr Ile Tyr Leu Leu Arg
35 40

(2) INFORMATION FOR SEQ ID NO:367:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 137 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

Met Lys His Phe Asp Thr Ile Val Ile Gly Gly Gly Pro Ala Gly Met
1 5 10 15
Met Ala Thr Ile Ser Ser Phe Tyr Gly Gln Lys Thr Leu Leu Ile
20 25 30
Glu Lys Asn Arg Lys Leu Gly Lys Lys Leu Ala Gly Thr Gly Gly
35 40 45
Arg Cys Asn Val Thr Asn Asn Gly Ser Leu Asp Asn Leu Leu Ala Gly
50 55 60
Ile Pro Gly Asn Gly Arg Phe Leu Tyr Ser Val Phe Ser Gln Phe Asp
65 70 75 80
Asn His Asp Ile Ile Asn Phe Phe Thr Glu Asn Gly Val Lys Leu Lys
85 90 95
Val Glu Asp His Gly Arg Val Phe Pro Ala Ser Asp Lys Ser Arg Thr
100 105 110
Ile Ile Glu Ala Leu Glu Lys Lys Ile Thr Glu Leu Gly Gly Gln Val
115 120 125

Ala Thr Pro Asn Arg Asn Arg Phe Cys
130 135

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

Met Thr Leu Ala Lys Asp Ile Ala Ser His Leu Leu Lys Ile Gln Ala
1 5 10 15
Val Tyr Leu Lys Pro Glu Glu Pro Phe Thr Trp Ala Ser Gly Ile Lys
20 25 30
Ser Pro Ile Tyr Thr Asp Asn Arg Val Thr Leu Ala Tyr Pro Glu Thr
35 40 45
Arg Thr Leu Ile Glu Asn Gly Phe Val Glu Ala Ile Lys Glu Ala Phe
50 55 60
Pro Glu Val Glu Val Ile Ala Gly Thr Ala Thr Ala Gly Ile Pro His
65 70 75 80
Gly Ala Ile Ile Ala Asp Lys Met Asp Leu Pro Phe Ala Tyr Ile Pro
85 90 95

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

Met Val Lys Val Leu Ala Ala Cys Gly Asn Gly Met Gly Ser Ser Met
1 5 10 15
Val Ile Lys Met Lys Val Glu Asn Ala Leu Arg Lys Leu Asn Gln Thr
20 25 30

Asp	Phe	Thr	Val	Asn	Ser	Cys	Ser	Val	Gly	Glu	Ala	Lys	Gly	Leu	Ala
35								40				45			
Val	Gly	Tyr	Asp	Ile	Val	Ile	Ala	Ser	Leu	His	Leu	Ile	Gln	Glu	Leu
50								55				60			
Glu	Gly	Arg	Thr	Asn	Gly	Lys	Leu	Ile	Gly	Leu	Asp	Asn	Leu	Met	Asp
65								70			75			80	
Asp	Lys	Glu	Ile	Thr	Glu	Lys	Leu	Ser	Gln	Ala	Ile	Gln			
					85					90					

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

Met	Ser	Met	Phe	Leu	Asp	Thr	Ala	Lys	Ile	Lys	Val	Lys	Ala	Gly	Asn
1				5					10					15	
Gly	Gly	Asp	Gly	Met	Val	Ala	Phe	Arg	Arg	Glu	Lys	Tyr	Val	Pro	Asn
				20				25				30			
Gly	Gly	Pro	Trp	Gly	Gly	Asp	Gly	Gly	Arg	Gly	Asn	Val	Val	Phe	
				35				40			45				
Val	Val	Asp	Glu	Gly	Leu	Arg	Thr	Leu	Met	Asp	Phe	Arg	Tyr	Asn	Arg
				50				55			60				
His	Phe	Lys	Ala	Asp	Ser	Gly	Glu	Lys	Gly	Met	Thr	Lys	Gly	Met	His
	65				70					75			80		
Gly	Arg	Gly	Ala	Glu	Asp	Leu	Arg	Val	Arg	Val	Pro	Gln	Gly	Thr	Thr
				85				90			95				
Val	Arg	Asp	Ala	Glu	Thr	Gly	Lys	Val	Leu	Thr	Asp	Leu	Ile	Glu	His
				100				105			110				
Gly	Gln	Glu	Phe	Ile	Val	Ala	His	Gly	Gly	Pro	Trp	Trp	Thr	Trp	Lys
				115				120			125				
Tyr	Ser	Phe	Arg	Asp	Thr	Lys	Lys	Ser	Cys	Thr	Gly	Asn	Leu		
				130				135			140				

(2) INFORMATION FOR SEQ ID NO:371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

```

Met Met Lys Gly Glu Met Thr Phe Lys Gln Val His Tyr Lys Tyr Gly
 1           5           10          15
Tyr Gly Arg Asp Val Leu Ser Asp Ile Asn Leu Thr Val Pro Gln Gly
 20          25          30
Ser Lys Val Ala Phe Val Gly Ile Ser Gly Ser Gly Lys Thr Thr Leu
 35          40          45
Ala Lys Met Met Val Asn Phe Tyr Asp Pro Ser Gln Gly Glu Ile Ser
 50          55          60
Leu Gly Gly Val Asn Leu Asn Gln Ile Asp Lys Lys Ala Leu Arg Gln
 65          70          75          80
Tyr Ile Ile Tyr Leu Pro Pro Gln Pro Tyr Val Phe Asn Gly Thr Ile
 85          90          95
Leu Glu Asn Leu Leu Gly Ala Lys Gly Gly Asp Asp Thr Gly Lys
100         105         110
Ile Ser Leu Thr Gly Arg Ser Glu Phe Gly Ser Glu Ile Pro Lys Arg
115         120         125
Asn Ile Ser Lys Pro Pro Cys His Leu Glu Ile Tyr Gln Thr Glu Leu
130         135         140
Thr Ser Asp Gly Ala Gly Ile Ser Gly Gly Gln Arg Gln Arg Ile Ala
145         150         155         160
Leu Ala Arg Ala Leu Leu Thr Asp Ala Pro Val Leu Ile Leu Asp Glu
165         170         175
Ala Thr Asn Ser Leu Asp Ile Leu Thr Lys Lys Arg Ile Val His Tyr
180         185         190
Leu Met Ala Leu Asp Lys Thr Phe Asp Phe His Cys Ser Pro Leu Asp
195         200         205
Tyr Cys
210

```

(2) INFORMATION FOR SEQ ID NO:372:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 73 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

Met Ala Arg Phe Ile Glu Ile Asp Ala Lys Glu His Asp Arg Val Thr
1 5 10 15
Ser Gln Ile Ser His Phe Pro His Ile Leu Ala Ser Ser Leu Met Glu
20 25 30
Gln Thr Ala Val Tyr Ala Gln Glu His Glu Asn Gly Lys Ala Leu Cys
35 40 45
Gly Arg Trp Phe Ser Arg Tyr Asp Pro Asn Cys Gly Lys Arg Ala Arg
50 55 60
Asn Val Asp Leu His Ser Leu Val Gln
65 70

(2) INFORMATION FOR SEQ ID NO:373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

Met Ala His Gln Gly Gln Asp Ile Tyr Asp Phe Pro Arg Ala Met Ile
1 5 10 15
Lys Glu Asp Asn Leu Glu Phe Ser Phe Ser Gly Leu Lys Ser Ala Phe
20 25 30
Ile Asn Leu His His Asn Ala Glu Gln Lys Gly Glu Ser Leu Ser Thr
35 40 45
Glu Asp Leu Cys Ala Ser Phe Gln Ala Ala Val Leu Asp Ile Leu Met
50 55 60
Ala Lys Thr Lys Lys Ala Leu Glu Lys Tyr Pro Val Lys Thr Leu Val
65 70 75 80
Val Ala Gly Gly Val Ala Ala Asn Lys Gly Leu Arg Glu Arg Leu Ala
85 90 95
Ala Glu Val Thr Asp Val Lys Val Ile Ile Pro Pro Leu Arg Leu Cys
100 105 110
Gly Asp Asn Ala Gly Met Ile Ala Tyr Ala Ser Val Ser Glu Trp Asn
115 120 125

Lys Glu Asn Phe Ala Asn Leu Asp Leu Asn Ala Lys Pro Ser Leu Ala
130 135 140
Phe Asp Thr Met Glu
145

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

Met Lys Arg Ser Leu Asp Ser Arg Val Asp Tyr Ser Leu Leu Leu Pro
1 5 10 15
Val Phe Phe Leu Leu Val Ile Gly Val Val Ala Ile Tyr Ile Ala Val
20 25 30
Ser His Asp Tyr Pro Asn Asn Ile Leu Pro Ile Leu Gly Gln Gln Val
35 40 45
Ala Trp Ile Ala Leu Gly Leu Val Ile Gly Phe Val Val Met Leu Phe
50 55 60
Asn Thr Glu Phe Leu Trp Lys Val Thr Pro Phe Leu Tyr Ile Phe Arg
65 70 75 80
Leu Gly Thr Tyr Asp Leu Ala Asp Cys Ile Leu
85 90

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

Met Pro Asp Asp Ile Ile Asp Ser Phe Trp Tyr Ile Ile Asp His Phe
1 5 10 15

Leu Lys Asn Val Phe Glu Leu Glu Glu Leu Glu Phe Gln Leu Leu
20 25 30
Asn Asn Gln Gly Lys Ile Thr Phe His Phe Ser Ser Gln His Leu Pro
35 40 45
Thr Ala Ile Asp Phe Asp Phe Asn His Pro Phe Asp Pro Arg Tyr Pro
50 55 60
Pro Arg Val Leu Val Leu Asp Met Asp Gly Arg Glu Thr Ile Leu Leu
65 70 75 80
Pro Glu Glu Asn Asp Leu Phe
85

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

Met Gly Lys Lys Asp Ala Ser Ala Met His Glu Met Arg Ala Ser Phe
1 5 10 15
Ile Gln Gly Ser Ile Glu Ala Gly His Thr Ala Glu Lys Ser Glu Gln
20 25 30
Val Phe Asp Val Met Glu Lys Phe Ala Gly Tyr Gly Phe Asn Arg Ser
35 40 45
His Ala Tyr Ala Tyr Ser Ala Leu Ala Phe Gln Leu Ala Tyr Phe Lys
50 55 60
Thr His Tyr Pro Ala Ile Phe Tyr Gln Val Met Leu Asn Tyr Ser Asn
65 70 75 80
Ser Asp Tyr Leu Ile Asp Ala Leu Glu Ala Gly Phe Glu Val Ala Ser
85 90 95
Leu Ser Ile Asn Thr Ile Pro Tyr His Asp Lys Ile Ala Asn Lys Ser
100 105 110
Ile Tyr Ile Gly Leu Lys Ser Ile Lys Gly Leu Gln Gln Gly Leu Gly
115 120 125
Ala Leu Asp Tyr
130

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

Met Asp Lys Lys Gln Asn Leu Thr Ser Phe Gln Glu Leu Thr Thr Thr
1 5 10 15
Glu Leu Asn Gln Ile Thr Gly Gly Glu Trp Trp Glu Glu Leu Leu His
20 25 30
Glu Thr Ile Leu Ser Lys Phe Lys Ile Thr Lys Ala Leu Glu Leu Pro
35 40 45
Ile Gln Leu
50

(2) INFORMATION FOR SEQ ID NO:378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

Met His Glu Met Phe Thr Ala Ile Ala Glu Ser Asp Met Lys Lys Ala
1 5 10 15
Ala Ala Ile Gln Arg Lys Phe Ile Pro Lys Val Asn Ala Leu Phe Ser
20 25 30
Tyr Pro Ser Pro Ala Pro Val Lys Ala Ile Leu Asn Tyr Met Gly Phe
35 40 45
Glu Ala Gly Pro Thr Arg Leu Pro Leu Val Pro Ala Pro Glu Glu Asp
50 55 60
Val Lys Arg Ile Ile Lys Val Val Val Asp Gly Asp Tyr Glu Ala Thr
65 70 75 80
Lys Ala Thr Val Thr Gly Val Leu Arg Pro Asp Tyr
85 90

(2) INFORMATION FOR SEQ ID NO:379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

Met Leu Asn Glu Phe Pro Ile Phe Asp Tyr Glu Asp Ile Gln Leu Ile
1 5 10 15
Pro Asn Lys Cys Val Ile Lys Ser Arg Ala Glu Ala Asp Thr Ser Val
20 25 30
Thr Leu Gly Asn His Thr Phe Lys Leu Pro Val Val Pro Ala Asn Met
35 40 45
Gln Thr Ile Leu Asp Glu Asn Val Ala Glu Gln Leu Ala Lys Gly Gly
50 55 60
Tyr Leu Tyr Thr Tyr Ala Pro Phe
65 70

(2) INFORMATION FOR SEQ ID NO:380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

Met Asp Ile Lys Leu Lys Asp Phe Glu Gly Pro Leu Asp Leu Leu
1 5 10 15
His Leu Val Ser Lys Tyr Gln Met Asp Ile Tyr Asp Val Pro Ile Thr
20 25 30
Glu Val Ile Glu Gln Tyr Leu Ala Tyr Val Ser Thr Leu Gln Ala Met
35 40 45
Arg Leu Glu Val Thr Gly Glu Tyr Met Val Met Ala Ser Gln Leu Met
50 55 60

Leu	Ile	Lys	Ser	Arg	Lys	Leu	Leu	Pro	Lys	Val	Ala	Glu	Val	Thr	Asp
65					70				75					80	
Leu	Gly	Asp	Asp	Leu	Glu	Gln	Asp	Leu	Leu	Ser	Gln	Ile	Glu	Glu	Tyr
					85				90				95		
Arg	Lys	Phe	Lys	Leu	Leu	Gly	Glu	His	Leu	Glu	Ala	Lys	His	Gln	Glu
					100			105				110			
Thr	Gly	Pro	Val	Leu	Phe	Gln	Ser	Ala	Asp	Arg	Val	Asp	Leu	Arg	Arg
					115			120			125				
Cys	Gly	Ala	Cys	Ala											
					130										

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

Met	Gln	Ser	Thr	Glu	Lys	Pro	Leu	Thr	Ala	Phe	Thr	Xaa	Ile	Ser	
1				5				10					15		
Thr	Ile	Ile	Leu	Leu	Leu	Leu	Thr	Val	Leu	Xaa	Ile	Phe	Pro	Phe	Tyr
								20		25			30		
Trp	Ile	Leu	Thr	Gly	Ala	Phe	Lys	Ser	Gln	Pro	Asp	Thr	Ile	Val	Ile
								35		40			45		
Pro	Pro	Gln	Trp	Phe	Pro	Lys	Met	Pro	Thr	Met	Glu	Asn	Phe	Gln	Gln
							50		55			60			
Leu	Met	Val	Gln	Asn	Pro	Ala	Leu	Gln	Trp	Met	Trp	Asn	Ser	Val	Phe
							65		70		75			80	
Ile	Ser	Leu	Val	Thr	Met	Phe	Leu	Val	Cys	Ala	Thr	Ser	Ser	Leu	Ala
							85		90			95			
Gly	Tyr	Val	Leu	Ala	Xaa	Lys	Arg	Phe	Tyr	Gly	Xaa	Arg	Ile	Tyr	Cys
							100		105			110			

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

Met Leu Phe Met Arg Asp Ser Leu Asp Ser Ile Val Glu Pro Val Leu
1 5 10 15
Asp Glu Met Gly Arg Phe Tyr Asp Trp Thr Glu Glu Lys Ala Thr
20 25 30
Tyr Arg Ala Asp Val Lys Ala Ala Leu Ala Gln Asn Asp Leu Ala Glu
35 40 45
Leu Lys Asn
50

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

Met Lys Ile Lys Val Val Thr Val Gly Lys Leu Lys Glu Lys Tyr Leu
1 5 10 15
Lys Asp Gly Ile Ala Glu Tyr Ser Lys Arg Ile Ser Arg Phe Ala Lys
20 25 30
Phe Glu Met Ile Glu Leu Ser Asp Glu Lys Thr Pro Asp Lys Ala Ser
35 40 45
Glu Ser Glu Asn Gln Lys Ile Leu Glu Ile Glu Gly Gln Arg Ile Leu
50 55 60
Ser Lys Ile Ala Asp Arg Asp Phe Val Ile Val Leu Ala Ile Glu Gly
65 70 75 80
Lys Thr Phe Phe Ser Glu Glu Phe Ser Lys Gln Leu Glu Glu Thr Ser
85 90 95
Ile Lys Gly Xaa Ser Thr Leu Thr Phe Ile Ile Gly Gly Ser Leu Gly
100 105 110
Leu Ser Ser Ser Val Lys Asn Arg Ala Asn Leu Ser Val Ser Phe Gly
115 120 125

Arg Leu Thr Leu Pro His Gln Leu Met Arg Leu Val Leu Val Glu Gln
130 135 140
Ile Tyr Arg Ala Phe Thr Ile Gln Gln Gly Phe Pro Tyr His Lys
145 150 155

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

Met Gly Ile Leu Ala Trp Cys Asp Leu Val Leu Tyr Arg Leu Trp Asp
1 5 10 15
Ser Phe Met Asp Leu Gly Leu Phe Ile Asn Asp Ala Trp Val Arg Lys
20 25 30
Lys Lys Thr Leu Asn Lys Glu Arg Lys Lys Ala Gly Lys Ala Ala Leu
35 40 45
Pro Glu Asn Arg Trp Ile Gln Leu Leu Gly Met Val Val Thr Phe His
50 55 60
Val Val Met Leu Ser Phe Leu Ile Phe Ser Gly Phe Leu Asn Asn Leu
65 70 75 80
Trp Phe Lys Lys

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

Met Val Met Ala Glu Asp Gln Ala Val Arg Gln Asn Arg Leu Ala Ile
1 5 10 15

Leu Ser Gln Leu Thr Lys Lys Ala Ala Lys Phe Ala Cys Phe Asn Gln
20 25 30
Ile Asn Thr Lys
35

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

Met Gly Ala Gln Pro Val Gln Asp Thr Glu Thr Ser Ser Ala Leu Ile
1 5 10 15
Ser Ser His Tyr Leu Asp Glu Gln Asp Leu Ser Glu Lys Leu Lys Ser
20 25 30
Glu Leu Gln Trp Phe Glu Leu Glu Asn Lys Leu Leu Asn Leu Trp Glu
35 40 45
His

(2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

Met Asp Glu Val Thr Ile Phe Gly Ile Asn Tyr Phe Lys Glu His Tyr
1 5 10 15
Pro Glu Lys Leu Ala Glu Arg Phe Lys Gln Met Lys Ile Glu Glu Glu
20 25 30
Ala Pro Val Ile Ile Met Asp Met Thr Arg Ala Leu Gly Phe Arg Asp
35 40 45

Asp Tyr Asp Arg Phe Tyr Ser Leu Phe Arg Glu Gly Ser Pro
50 55 60

(2) INFORMATION FOR SEQ ID NO:388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

Met Lys Val Ile Asn Gln Thr Leu Leu Glu Lys Val Ile Ile Glu Arg
1 5 10 15
Ser Arg Ser Ser His Lys Gly Asp Tyr Gly Xaa Leu Leu Leu Leu Gly
20 25 30
Gly Thr Tyr Pro Tyr Gly Val Xaa Ser Ser Trp Leu Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

Met Asn Trp Ile Leu Leu Gln Gly Leu Ile Cys Gln Arg Asp Ala Ser
1 5 10 15
Tyr Asp Met Lys Gln Asp Asp Leu Asp Lys Val Ala Asp Tyr Leu Phe
20 25 30
Lys Thr Glu Glu Trp Thr Met Tyr Glu Leu Ile Leu Phe Gly Asn Leu
35 40 45
Tyr Ser Phe Tyr Asp Val Asp Tyr Val Thr Arg Ile Gly Arg Glu Val
50 55 60
Met Glu Arg Glu Glu Phe Tyr Gln Glu Ile Ser Arg His Lys Arg Leu
65 70 75 80

Val	Leu	Ile	Leu	Ala	Leu	Asn	Cys	Tyr	Gln	His	Cys	Leu	Glu	His	Ser
						85			90					95	
Ser	Phe	Tyr	Asn	Ala	Asn	Tyr	Phe	Glu	Ala	Tyr	Thr	Glu	Lys	Ile	Ile
						100			105				110		
Asp	Lys	Gly	Ile	Lys	Leu	Tyr	Glu	Arg	Asn	Val	Phe	His	Tyr	Leu	Lys
						115			120			125			
Gly	Phe	Ala	Leu	Tyr	Gln	Lys	Gly	Gln	Cys	Lys	Glu	Gly	Cys	Lys	Gln
						130			135			140			
Met	Gln	Glu	Thr	Met	His	Ile	Phe	Asp	Val	Leu	Gly	Leu	Pro	Glu	Gln
						145			150			155		160	
Val	Ser	Leu	Leu	Ser	Gly	Thr	Leu	Arg	Lys	Ile	Cys	Gln	Lys	Leu	Ile
						165			170			175			
Phe	Pro	Asn	Lys	Gly	Lys	Asn	Lys	Lys	Leu	Leu	Ser	Val	Leu	Ile	Gln
						180			185			190			

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

Met	Ser	Thr	Val	Leu	Ser	Trp	Thr	Ala	Tyr	Lys	Thr	Gln	Arg	Leu	Glu
1						5				10			15		
Met	Ser	Ile	Leu	Leu	His	Met	Ile	Val	Asn	Gly	Ile	Ala	Phe	Cys	Leu
						20				25			30		
Leu	Ala	Leu	Val	Val	Ile	Met	Ser	Arg	Thr	Leu	Gly	Ile	Ser	Val	
						35				40			45		

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

Met Arg Glu Asn Asp Leu Leu Leu Ile Thr Ala Asp His Gly Asn Asp
1 5 10 15
Pro Thr Tyr Ala Gly Thr Asp His Thr Arg Glu Tyr Ile Pro Leu Leu
20 25 30
Ala Tyr Ser Pro Ala Phe Lys Gly Asn Gly Leu Ile Pro Val Gly His
35 40 45
Phe Ala Asp Ile Ser Ala Thr Val Ala Asp Asn Phe Gly Val Glu Thr
50 55 60
Ala Met Ile Gly Glu Ser Phe Leu Asp Lys Leu Val
65 70 75

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

Met Lys Lys Ile Phe Leu Thr Leu Leu Thr Val Ser Leu Leu Gly Gly
1 5 10 15
Ala Ser Thr Ala Val Ala Gln Asp Phe Thr Ile Ala Ala Lys His Ala
20 25 30
Ile Ala Val Glu Ala Asn Thr Gly Lys Ile Leu Tyr Glu Lys Asp Ala
35 40 45
Thr Pro Pro Val Glu Ile Ala Ser Ile Thr Lys Leu Ile Thr Val Tyr
50 55 60
Leu Val Tyr Glu Ala Leu Glu Asn Gly Ser Ile Thr Leu Ser Thr Pro
65 70 75 80
Val Asp Ile Ser Asp Tyr Pro Tyr Gln Leu Thr Thr Asn Ser Glu Ala
85 90 95
Ser Asn Ile Pro Met Glu Ala Arg Asn Tyr Thr Val Glu Glu Leu Leu
100 105 110
Glu Ala Thr Leu Val Ser Ser Ala Asn Ser Ala Ala Ile Ala Leu Ala
115 120 125
Glu Lys Ile Ala Gly Ser Glu Lys Asp Phe Val Xaa Met Met Arg Ala
130 135 140

Lys Leu Leu Glu Trp Gly Ile Arg Ile His Cys Cys Gln Tyr Asp Arg
145 150 155 160
Ser

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

Met Ser Asn Ala Met Glu Gly Val Leu Tyr Phe Leu Lys Pro Asp Phe
1 5 10 15
Ser Lys Leu Thr Ser Ala Asp Leu Leu Tyr Ala Leu Gly Gln Ser Phe
20 25 30
Phe Ala Leu Ser Leu Gly Val Thr Asp Met Leu Thr Tyr Ala Ser Tyr
35 40 45
Leu Asp Lys Lys Thr Asn Leu Val Gln Ser Gly Ile Ser Ile Val Thr
50 55 60
Met Asn Ile Ser Ile Val His His Gly Arg Ser Ser His Phe Pro Ser
65 70 75 80
His Val Ser Leu Gln Tyr Pro Leu
85

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

Met Lys Val Ala Lys Pro Phe Trp Ala Ile Val Lys Leu Lys Ser Val
1 5 10 15

Gln	His	Ala	Ser	Met	Leu	Glu	Asn	Pro	Lys	Glu	Met	Asp	Gly	Leu	Met
				20				25			30				
Lys	Gln	Val	Glu	Asn	Leu	Ala	Leu	Glu	Asn	Gln	Gly	Tyr	Gln	Val	Glu
				35			40			45					
Lys	Glu	Asn	Lys	Ala	Phe	Glu	Gln	Ile	Lys	Asp	Ser	Val	Ala	Thr	Phe
				50			55			60					
Gln	Thr	Phe	Leu	Thr	Ile	Phe	Leu	Tyr	Gly	Cys					
				65			70			75					

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

Met	Asp	Ala	Glu	Val	Ser	Lys	Asn	Leu	Arg	Leu	Ile	Leu	Glu	Arg	Lys
1				5				10			15				
Gly	Met	Thr	Ile	Leu	Thr	Gly	Thr	Lys	Leu	Gln	Glu	Ile	Ile	Glu	Glu
				20			25			30					
Asn	Gly	Gln	Leu	Arg	Ile	Lys	Val	Glu	Gly	Lys	Asp	Asn	Ile	Ile	Ala
				35			40			45					
Ser	Lys	Ala	Leu	Leu	Ser	Ile	Gly	Arg	Met	Pro	Asp	Leu	Glu	Gly	Ile
				50			55			60					
Gly	Glu	Val	Glu	Phe	Glu	Leu	Asp	Arg	Gly	Cys	Ile	Lys	Val	Asn	Glu
				65			70			75			80		
Tyr	Met	Glu	Thr	Ser	Val	Pro	Arg	Ile	Tyr	Ala	Thr	Arg			
				85				90							

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

Met Lys Asn Ser Ile Met Asp Thr Lys Phe Asp Arg Arg Ile Leu Leu
1 5 10 15
Leu Asn Lys Ile Ile Ile Val Phe Ile Val Leu Met Thr Leu Leu Pro
20 25 30
Leu Leu Tyr Ile Val Val Ala Ser Phe Met Asp Pro Lys Val Leu Val
35 40 45
Ser Arg Gly Ile Ser Phe Asn Pro Ala Asp Trp Thr Val Glu Gly Tyr
50 55 60
Gln Arg Val Ile Gln
65

(2) INFORMATION FOR SEQ ID NO:397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

Met Val Ile Pro Glu Ala Gly Tyr Leu Tyr Ala Phe His Tyr Pro Asn
1 5 10 15
Leu Lys Gly Lys Gly Lys Glu Ala Val Gln Val Ile Tyr Asn Leu Asn
20 25 30
Leu Ala Ser Ala Lys Val Ile Gln Leu Tyr Arg Ser Leu Gly Leu Asp
35 40 45
Gly Lys Ile Gly Ile Ile Leu Asn Leu Thr Pro Ala Tyr Pro Arg Ser
50 55 60
Asn Ser Pro Glu Asp Leu Glu Ala Ser Arg Phe Thr Asp Asp Phe Phe
65 70 75 80
Asn Lys Val Phe Leu Glu Ser Ser Cys
85

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

Met	Thr	Arg	Ile	Ala	Ser	Val	Ser	Val	Ile	Arg	Asn	Ala	Ala	Phe	Ile
1									10						15
Ala	Ile	Ala	Leu	Ser	Phe	Leu	Gly	Lys	Phe	Thr	Ala	Leu	Ile	Ser	Thr
			20					25						30	
Ile	Pro	Asn	Ala	Val	Leu	Gly	Gly	Met	Ser	Ile	Leu	Leu	Tyr	Gly	Val
								35	40					45	
Ile	Ala	Ser	Asn	Gly	Leu	Lys	Val	Leu	Ile	Lys	Glu	Arg	Val	Asp	Phe
			50				55				60				
Ala	Gln	Met	Arg	Asn	Leu	Ile	Ile	Ala	Ser	Ala	Met	Leu	Val	Leu	Gly
						65					75				80
Leu	Gly	Arg	Ser	Tyr	Pro										
					85										

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

Met	Ser	Leu	Arg	Glu	Lys	Ser	Met	Ser	Glu	Tyr	Lys	Leu	Ser	Glu	Asn
1							5			10					15
Asn	Trp	Thr	Arg	Val	Ala	Val	Phe	Ala	Gly	Gly	Asn	Arg	Gly	His	Tyr
							20			25				30	
Arg	Thr	Asp	Phe	Asp	Ala	Phe	Val	Gly	Val	Asp	Arg	Gly	Ser	Leu	Trp
							35			40			45		
Val	Leu	Glu	Glu	Asp	Leu	Pro	Leu	Ala	Leu	Ala	Val	Gly	Asp	Phe	Asp
							50			55			60		
Ser	Val	Thr	Glu	Glu	Glu	Arg	Gln	Val	Ile	Gln	Lys	Arg	Ala	Gln	Tyr
							65			70			75		80
Phe	Val	Gln	Ala	Arg	Pro	Glu	Lys	Asp	Asp	Thr	Asp	Leu	Glu	Leu	Ala
							85			90				95	

Leu Leu Thr Ile Phe Glu Gln Asn Pro Gln Ala Glu Val Thr Ile Phe
100 105 110
Gly Ala Leu Gly Gly Arg Ile Asp His Met Leu Ala Asn Val Leu Ser
115 120 125
Thr

(2) INFORMATION FOR SEQ ID NO:400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

Met Val Leu Gln Arg Asn Glu Ile Asn Glu Lys Asp Thr Trp Asp Leu
1 5 10 15
Ser Thr Ile Tyr Pro Thr Asp Gln Ala Trp Glu Glu Ala Leu Lys Asp
20 25 30
Leu Thr Glu Gln Leu Glu Thr Val Ala Gln Tyr Glu Gly His Leu Leu
35 40 45
Asp Ser Ala Asp Asn Leu Leu Val Asn His
50 55

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

Met Ile Tyr Gly Ala Ile Ile Asp Ala Lys Thr Ala Glu Asn Ala Ala
1 5 10 15
Gly Met Thr Ala Met Gln Thr Ala Thr Asp Asn Ala Lys Lys Val Ile
20 25 30
301

Asn Asp Leu Thr Ile Gln Tyr Asn Arg Ala Gln Thr Gly Gly Tyr Tyr
35 40 45
Thr Arg Asn Tyr Arg Asn Arg Ser Ser Ala
50 55

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

Met Thr Asp Gly Tyr Glu His Tyr Lys Lys Ile Met Glu Asn Pro Pro
1 5 10 15
Lys Asn Leu Ile Phe Pro Gly Ile Val Ser Pro Glu Arg Met Arg Glu
20 25 30
Ile Val Cys Ser Asn Gly Ser Phe Leu Val Ala
35 40

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

Met Ser Lys Gln Lys Lys Phe Glu Glu Asn Leu Ala Glu Leu Glu Thr
1 5 10 15
Ile Val Gln Ser Leu Glu Asn Gly Glu Ile Ala Leu Glu Asp Ala Ile
20 25 30
Thr Ala Phe Gln Lys Gly Met Val Leu Ser Lys Glu Leu Gln Ala Thr
35 40 45
Leu Asp Lys Ala Glu Lys Thr Leu Val Lys Val Met Gln Glu Asp Gly
50 55 60

Thr Glu Ser Asp Phe Glu
65 70

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

Met Phe Ala Ala Val Thr Ala Gly Tyr Gln Ala Ala Leu Met Val Pro
1 5 10 15
Thr Glu Ile Leu Ala Glu Gln His Phe Glu Ser Leu Gln Asn Leu Phe
20 25 30
Pro Asn Leu Lys Leu Ala Leu Leu Thr Gly Ser Leu Lys Ala Ala Glu
35 40 45
Lys Arg Glu Val Leu Glu Thr Ile Ala Lys Gly Glu Ala Asp Leu Ile
50 55 60
Ile Gly Thr His Ala Leu Ile Gln Asp Gly Val Glu Tyr Ala Arg Leu
65 70 75 80
Gly Leu Ile Ile Ile Asp Glu Gln His Arg Phe Gly Val Gly Gln Arg
85 90 95
Arg Ile Leu Arg Glu Lys Gly Asp Asn Pro Asp Val Leu Met Met Thr
100 105 110
Ala Thr Pro Ile Pro Arg Thr Leu Ala Ile Thr Ala Phe Gly Asp Met
115 120 125
Asp Val Ser Ile Ile Asp Gln Met Pro Ala Gly Arg Lys Pro Tyr Cys
130 135 140
Asp Ala Leu Asp Gln Thr
145 150

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

Met Asn Arg Glu Ala Leu Arg Leu Tyr Leu Val Thr Asn Arg Tyr Gln
1 5 10 15
Asp Ser Val Glu Ser Phe Leu Ala Lys Val Glu Thr Ala Cys Arg Ser
20 25 30
Gly Val Thr Ile Val Gln Leu Arg Glu Lys Asn Leu Thr Thr Asn Gln
35 40 45
Tyr Tyr Gln Leu Ala Lys Gln Val Lys Glu Ile Thr Asp Ala Tyr Gln
50 55 60
Val Pro Leu Ile Ile Asp Asp Arg Leu Asp Val Cys Leu Ala Val Asp
65 70 75 80
Ala Ala Gly Leu His Ile Gly Asp Asp Glu Leu Pro Val Ser Val Ala
85 90 95
Arg Gln Val Leu Gly Pro Glu Lys Ile Pro Arg Cys His Arg
100 105 110

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

Met Gln Gly Ser His Phe His Leu Pro Ile Tyr Arg Met Thr Ser Gln
1 5 10 15
Ala Leu Leu Asp Glu Thr Lys Lys Val Ala Ile Pro Val Leu Ala Thr
20 25 30
Thr Gln Ser Lys Asp Ser Val Asp Tyr Arg Glu Leu Pro Ser Ile Glu
35 40 45
Asn Phe Val Leu Val Met Gly Asn Glu Gly Gln Gly Ile Ser Pro Leu
50 55 60
Met Ala Glu Ser Ala Asp Gln Leu Val His Ile Ser Met Lys Gly Gln
65 70 75 80
Ala Glu Ser Leu Asn Val Ala Val Ala Ala Gly Ile Leu Ile Phe His
85 90 95
Leu Ser

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

Met	Thr	Lys	Thr	Ala	Phe	Leu	Phe	Ala	Gly	Gln	Gly	Ala	Gln	Tyr	Leu
1					5				10					15	
Arg	Met	Gly	Arg	Asp	Phe	Tyr	Asp	Gln	Tyr	Pro	Ile	Val	Lys	Glu	Thr
					20				25					30	
Ile	Asp	Arg	Ala	Ser	Gln	Val	Leu	Gly	Tyr	Asp	Leu	Arg	Tyr	Leu	Ile
					35			40				45			
Asp	Thr	Glu	Glu	Asp	Lys	Leu	Asn	Gln	Thr	Arg	Tyr	Thr	Gln	Pro	Ala
					50			55			60				
Ile	Leu	Ala	Thr	Ser	Val	Ala	Ile	Tyr	Arg	Leu	Leu	Gln	Glu	Lys	Gly
					65			70			75			80	
Tyr	His	Pro	Asp	Met	Val	Ala	Gly	Leu	Ser	Leu	Gly	Glu	Tyr	Ser	Ala
					85				90				95		
Leu	Val	Ala	Ser	Gly	Ala	Leu	Asp	Phe	Glu	Asp	Ala	Val	Ala	Leu	Val
					100			105				110			
Ala	Lys	Arg	Gly	Ala	Tyr	Met	Glu	Glu	Ala	Ala	Pro	Ala	Asp	Ser	Gly
					115			120				125			
Lys	Met	Val	Ala	Val	Leu	His	Thr	Pro							
					130			135							

(2) INFORMATION FOR SEQ ID NO:408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

Met Tyr Gln Phe Ser Gly Gln Thr Lys Val Xaa Glu Val Leu Ala Phe
1 5 10 15
Arg Asp Lys Pro Pro Tyr Gly Gly Ser Ser Ala Met Pro Leu Arg Cys
20 25 30
Leu

(2) INFORMATION FOR SEQ ID NO:409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

Met Thr Lys Glu Thr Gly Met Glu Gln Thr Phe Phe Ile Ile Lys Pro
1 5 10 15
Asp Gly Val Lys Arg Gly Leu Val Gly Glu Val Leu Lys Arg Ile Glu
20 25 30
Gln Arg Gly Phe Thr Ile Glu Lys Leu Glu Phe Arg Ser Gln Val Phe
35 40 45
Arg Arg Val Asp
50

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

Met Thr Ser Gly Pro Val Leu Val Gly Val Ile Ser Gly Pro Lys Val
1 5 10 15

Ile Glu Thr Trp Arg Thr Met Met Gly Ala Thr Arg Pro Glu Glu Ala
20 25 30
Leu Pro Gly Thr Ile Arg Gly Asp Phe Ala Lys Ala Ala Gly Glu Asn
35 40 45
Glu Ile Ile Gln Asn Val Val His Gly Ser Asp Ser Glu Lys Asn Gln
50 55 60
Leu Ser Arg Glu Ile Ala Pro Leu Val Leu Arg Val Asp Trp Leu Asn
65 70 75 80
Gln Leu Asp Lys Ser Ser Phe Glu
85

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

Met Gly Leu Lys Asp Asn Ala Gly Leu Val Lys Glu Tyr Ala Leu Val
1 5 10 15
Asp Ala Val Glu Tyr Gln Asn Val Ile Val Ala Thr Thr Val Glu Glu
20 25 30
Met Leu Ser Lys Tyr Ala Asn Lys Asn Asp Leu Glu Ile Asp Asn Ala
35 40 45
Thr Thr Glu Ser Ile Lys Gly Val Val Ala Asp Leu Lys Ser Ala Val
50 55 60
Ile Lys Gly Asp Thr Val Tyr Phe Phe Lys Val Asp Gly Lys Ile Tyr
65 70 75 80
Lys Val Lys Ala Ser Val Ser Asp Asp Leu Pro Tyr Leu Glu Asn Gly
85 90 95
Lys Thr Phe Glu Gly Gln Val Xaa Lys Asp Asn Tyr Leu Lys Thr Phe
100 105 110
Lys Val Gln
115

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

Met Ile Ser Gly Ser Glu Ile Arg Asp Ile Val Thr Ser Asp Ile Pro
1 5 10 15
Leu Ala Asp Lys Thr Glu Thr Leu Val Arg Phe Ala Asn Asn Ala Gly
20 25 30
Gly Leu Asp Asn Ile Thr Val Ala Leu Val Ser Met Asn Glu Glu Asp
35 40 45
Glu Glu
50

(2) INFORMATION FOR SEQ ID NO:413:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 76 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

Met Pro Asp Asn Leu Ala Leu Arg Met Arg Pro Lys Thr Ile Asp Gln
1 5 10 15
Val Ile Gly Gln Glu Xaa Leu Val Gly Pro Gly Lys Ile Ile Arg Arg
20 25 30
Met Val Glu Ala Asn Arg Leu Ser Ser Met Ile Leu Tyr Gly Pro Pro
35 40 45
Gly Ile Gly Lys Thr Ser Ile Ala Ser Ala Ile Ala Gly Thr Thr Lys
50 55 60
Tyr Ala Phe Arg Thr Phe Asn Ala Thr Val Asp Ser
65 70 75

(2) INFORMATION FOR SEQ ID NO:414:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 33 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

Met Pro Glu Glu Leu Ala Tyr Leu Val Gln His Leu Asp Asn Ala Gln
1 5 10 15
Glu Gln Val Val Leu Gly Asn Thr Tyr His Thr Gly Asn His Cys Phe
20 25 30
Ser

(2) INFORMATION FOR SEQ ID NO:415:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 45 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

Met Val Phe Trp Glu Gly Leu Val Pro Thr Pro Asp Val Ile Asp Ala
1 5 10 15
Gly His Val Thr Gly Phe Leu Tyr Thr Val His Ser Ser Ser Thr Gly
20 25 30
Leu Ile Val Leu Gln Ile Lys Lys Asp Leu Leu Lys Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:416:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 143 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

Met Thr Asp Arg Tyr Asp Ser Ser Leu Gly Ile Tyr Lys Val Pro Trp
1 5 10 15
Cys Val Ser Gln Gln Gln Thr Val Thr Glu Ile Met Asp Thr Tyr Cys
20 25 30
Asp Trp Gly Val Lys Tyr Pro Leu Val Tyr Leu Glu Asp Pro Phe Ser
35 40 45
Asp Glu Asp Leu Asp Ser Trp Arg Lys Phe Gln Leu Ile Lys Pro Leu
50 55 60
Lys Leu Gln Val Phe Gly Asp Asp Phe Tyr Ala Thr Asn Leu Glu Arg
65 70 75 80
Ile Ser Gln Phe Lys Asp Cys Ala Asp Gly Ile Val Ile Lys Pro Asn
85 90 95
Gln Val Gly Ser Val Ser Lys Thr Leu Glu Val Met Glu Tyr Ala Glu
100 105 110
Lys Ser Gly Ile Ser Met Ala Phe Ser Gln Arg Thr Ala Glu Thr Glu
115 120 125
Asn Asn Ile Ile Ser His Leu Ala Met Ser Val Ile Leu Leu Ile
130 135 140

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

Met Lys Lys Ile Ser Lys Gln Glu Leu Val Asn Thr Arg Phe Ser Arg
1 5 10 15
Leu Phe Ala His Phe Gly Gln Glu Lys Asp Gly Ser Phe Leu Ala Gln
20 25 30
Arg Tyr Gln Phe Tyr Leu Ala Gln Gln Gly Gln Thr Leu Ser Gly Ala
35 40 45
His Asp Leu Leu Asp Ser Leu Ile Glu Arg Asp Tyr Asn Leu Tyr Ala
50 55 60
Ala Thr Asn Gly Ile Thr Ala Ile Gln Thr Gly Arg Leu Ala Gln Ser
65 70 75 80

Gly	Leu	Ala	Pro	Tyr	Phe	Asn	Gln	Val	Phe	Ile	Ser	Glu	Gln	Leu	Gln
					85					90					95
Thr	Gln	Lys	Pro	Asp	Ala	Leu	Phe	Tyr	Glu	Lys	Ile	Gly	Gln	Gln	Ile
					100				105						110
Ala	Gly	Phe	Ser	Lys	Glu	Lys	Thr								
					115					120					

(2) INFORMATION FOR SEQ ID NO:418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

Met	His	Arg	Lys	Thr	Val	Ile	Asp	Xaa	Arg	Thr	Leu	Gly	Glu	Arg	Tyr
					1	5			10						15
Thr	Phe	Thr	Xaa	Pro	Ile	Lys	Glu	Leu	Lys	Thr	Arg	Asn	Val	Ala	Glu
					20			25						30	
Val	Ala	Asp	Leu	Leu	Ala	Xaa	Val	Glu	Ser	Tyr	Gln	Glu	Gln	Asp	Tyr
					35			40			45				
Tyr	Val	Val	Gly	Tyr	Val	Ser	Tyr	Glu	Ala	Ala	Pro	Ala	Phe	Glu	Glu
					50			55			60				
Lys	Leu	Ala	Val	His	Lys	Val	Pro	Leu	Leu	Gly	Glu	Tyr	Leu	Leu	Tyr
					65		70			75			80		
Phe	Thr	Val	His	Asp	Arg	Val	Glu	Thr	Ser	Pro	Ile	Pro	Leu	Thr	Tyr
					85			90			95				
Glu	Asp	Ile	Asp	Leu	Pro	Ser	Asn	Trp	Gln	Gly	Xaa	Asn	Val	Cys	Thr
					100			105			110				
Glu	Leu														

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

Met Glu Arg Ile Glu Val Arg Ser Arg Ser Gly Ser Ala His Leu Gly
1 5 10 15
His Val Phe Thr Asp Gly Pro Arg Glu Leu Gly Gly Leu Arg Tyr Cys
20 25 30
Ile Asn Ser Ala Ser Leu Arg Phe Val Ala Lys Asp Glu Met Glu Lys
35 40 45
Ala Gly Tyr Gly Tyr Leu Leu Pro Tyr Leu Asn Lys
50 55 60

(2) INFORMATION FOR SEQ ID NO:420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

Met Glu Trp Ile Arg Leu Ile Gly Ile Ala Ile Ile Val Val Gly Phe
1 5 10 15
Ile Leu Lys Phe Asp Thr Ile Ala Thr Val Val Leu Ala Gly Leu Val
20 25 30
Thr Ala Leu Val Ser Gly Val Ser Leu Val Glu Phe Leu Glu Ile Leu
35 40 45
Gly Lys Glu Phe Ser Asn Gln Arg Val Leu Thr Ile Phe Met Val Thr
50 55 60
Leu Pro Leu Val Gly Leu Ser Glu Thr Phe Gly Leu Asn Asn Asp Gln
65 70 75 80
Ser Ile

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

Met Leu Leu Ile Phe Ala Val Ile Gly Val Leu Val Ala Leu Ile Ala
1 5 10 15
Gln Phe Tyr Ser Ala Lys Ala Ala Val Gly Phe Ala Lys Glu Leu Thr
20 25 30
Asn Asp Leu Tyr Arg His Ile Leu Ser Leu Pro Lys Asp Ser Arg Asp
35 40 45
Arg Leu Thr Thr Ser Ser Leu Val Thr Arg Leu Thr Ser Asp Thr Tyr
50 55 60
Gln Ile Gln Thr Gly Ile Asn Gln Phe Leu Arg Leu Phe Leu Arg Ala
65 70 75 80
Pro Ile Ile Val Phe Gly Ala Ile Phe Met Ala Tyr Arg Ile Ser Ala
85 90 95
Glu Leu Thr Phe Trp Phe Leu Val Met Val Ala Ile Leu Thr Ile Val
100 105 110
Ile Val Arg Val Ile Ser Ile Gly Gln Ser Ser Leu Gln
115 120 125

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

Met Pro Ile Glu Gln Val Gln Lys Leu Leu Gly His Ser Lys Ile Asp
1 5 10 15
Thr Thr Leu Ala Tyr Ala Met Val Asn Gln Asn Asn Val Lys His Ser
20 25 30
His Gln Lys Phe Ile Ser
35

(2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

Met	Lys	Pro	Cys	Trp	Lys	Lys	Cys	Phe	Pro	Glu	Glu	Val	Ser	Ser	Glu
1					5					10					15
Gly	Glu	Val	Thr	Leu	Ile	Glu	Ile	Pro	Val	Ser	Asp	Lys	Ile	Ala	Gly
			20						25					30	
Lys	Gln	Val	His	Glu	Leu	Asn	Leu	Pro	His	Asn	Val	Leu	Ile	Thr	Thr
			35						40					45	
Gln	Val	His	Asn	Gly	Lys	Ser	Gln	Thr	Val	Asn	Gly	Ser	Thr	Arg	Met
			50						55					60	
Tyr	Leu	Gly	Asp	Met	Ile	His	Leu	Val	Ile	Pro	Lys	Ser	Glu	Ile	Gly
			65						70					75	
Lys	Val	Lys	Asp	Leu	Leu	Leu									80
							85								

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

Met	Asn	Glu	Gly	Val	Glu	Asn	Phe	Arg	Ala	Lys	Leu	Ala	Ser	Leu	Gly
1					5					10					15
Ala	Lys	Asn	Ile	Gly	Ile	Tyr	Val	Gly	Val	Tyr	Phe	Met	Glu	Glu	His
			20						25					30	
Ser	Ile	Asp	Thr	Gly	Lys	Phe	Thr	Ser	Val	Trp	Ile	Pro	Ser	Tyr	Gly
			35						40					45	
Ser	Asp	Ser	Gly	Phe	Leu	Glu	Ser	Ser	Pro	Lys	Thr	Asp	Leu	Asp	Tyr
			50						55					60	

Asp Ile His Gln Tyr Thr Ser Lys Gly Lys Leu Pro Ala Leu Thr Thr
65 70 75 80
Ile

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

Met Val Ser Lys Tyr Leu Leu Leu Ala Val Ile Phe Ser Gly Leu Val
1 5 10 15
Thr Trp Ile Leu Arg Met Ile Ser Phe Ile Leu Val Lys Tyr Lys Gly
20 25 30
Leu Pro Ala Ile Val Glu Arg Phe Leu Lys Phe Leu Pro Val Ser Ile
35 40 45
Ile Phe Ala Leu Ile Leu Ser Ser Val Val Thr Gly Lys Val Gly Ser
50 55 60
Leu Pro Gln Ile Lys Trp Leu Asp Phe Leu Ala Val Phe Pro Thr Ala
65 70 75 80
Trp Val Ala Phe Arg Tyr Arg Asn Leu Leu Gly Thr Val Leu Phe Gly
85 90 95
Val Val Leu Ile Ala Ile Leu Arg Leu Val Ser
100 105

(2) INFORMATION FOR SEQ ID NO:426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

Met Glu Asp Xaa Glu Thr Gln Arg Val Val Met Gln Tyr Arg Ala Pro
 1 5 10 15
 Glu Asn Asn Arg Trp Ser Gly Tyr Ala Phe Pro Gly Gly His Val Glu
 20 25 30
 Asn Asp Glu Ala Phe Ala Glu Ser Val Ile Arg Glu Ile Tyr Glu Glu
 35 40 45
 Thr Gly Leu Thr Ile Gln Asn Pro Gln Leu Val Gly Ile Lys Asn Trp
 50 55 60
 Pro Leu Asp Thr Gly Gly Arg Tyr Ile Val Ile Cys Tyr Lys Ala Thr
 65 70 75 80
 Glu Phe Ser Gly Thr Leu Gln Ser Ser Glu Glu Gly Glu Val Ser Trp
 85 90 95
 Val Gln Lys Asp Gln Ile Pro Asn Leu Asn Leu Ala Tyr Asp Met Leu
 100 105 110
 Pro Leu Met Glu Met Met Glu Ala Pro Asp Lys Ser Glu Phe Phe Tyr
 115 120 125
 Pro Arg Arg Thr Glu Asp Asp Trp Glu Lys Lys Ile Phe
 130 135 140

(2) INFORMATION FOR SEQ ID NO:427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

Met Thr Ile Glu Leu Leu Thr Pro Phe Thr Lys Val Glu Leu Glu Pro
 1 5 10 15
 Glu Ile Lys Glu Lys Lys Arg Lys Gln Val Gly Ile Leu Gly Gly Asn
 20 25 30
 Phe Asn Pro Val His Asn Ala His Leu Ile Val Ala Asp Gln Val Arg
 35 40 45
 Gln Gln Leu Gly Leu Asp Gln Val Leu Leu Met Pro Glu Tyr Gln Pro
 50 55 60
 Pro His Val
 65

(2) INFORMATION FOR SEQ ID NO:428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

Met Lys Lys Leu Val Phe Val Cys Leu Gly Asn Ile Cys Arg Ser Pro
1 5 10 15
Met Ala Glu Phe Val Met Lys Ser Met Thr Asp Asn Tyr Glu Ile Gln
20 25 30
Ser Arg Ala Thr Ser Ser Trp Glu His Gly Asn Pro Ile His Lys Gly
35 40 45
Thr Gln Gly Ile Phe Gln Glu Tyr Glu Ile Pro Tyr Asp Lys Asn Lys
50 55 60
Thr Ser Leu Gln Ile Ser Lys Glu Asp Phe Glu Ala Phe Asp Tyr Ile
65 70 75 80
Ile Gly Met Asp Ala Ser Asn Val Pro Thr Tyr Val Arg Cys Val Gln
85 90 95

(2) INFORMATION FOR SEQ ID NO:429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

Met Val Lys Tyr Gly Val Val Gly Ala Gly Tyr Phe Gly Ala Glu Leu
1 5 10 15
Ala Arg Tyr Met Gln Lys Asn Asp Gly Ala Xaa Ile Thr Leu Leu Tyr
20 25 30
Asp Pro Asp Asn Ala Glu Ala Ile Ala Glu Glu Leu Gly Ala Lys Val
35 40 45
Ser Lys Phe Leu Arg
50

(2) INFORMATION FOR SEQ ID NO:430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

Met Leu Trp Lys Tyr Tyr Asn Ser Ser Phe Leu Lys Ala Val Pro His
1 5 10 15
Leu Thr Thr Glu Tyr Lys Arg Leu Ala Gln Ala His Gly Leu Asn Leu
20 25 30
Lys Gln Ala Lys Pro Ile Thr Met Gly Met Trp Ile Gly Gly Asp Arg
35 40 45
Glu Gly Asn Pro Phe Val Thr Ala Lys Asn Leu Lys Gln Ser Ala Leu
50 55 60
Thr Gln Cys Glu Val Xaa Leu Asn Leu Leu
65 70

(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

Met Asn Thr Leu Tyr Leu Asn Gln His Ser Ser Tyr Lys Asn Asp Glu
1 5 10 15
Asp Ser His Ser Phe Pro Ile Gln Met Glu Leu Val Ser Asp Glu Met
20 25 30
Ile Pro Arg Asn
35

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

Met	Ala	Arg	Lys	Glu	Thr	Met	Ala	Glu	Arg	Lys	Tyr	Cys	Lys	Met	Lys
1				5				10						15	
Lys	Asp	Ile	His	Pro	Glu	Tyr	Arg	Pro	Val	Val	Phe	Met	Asp	Thr	Thr
					20				25					30	
Thr	Gly	Tyr	Gln	Phe	Leu	Ser	Gly	Ser	Thr	Lys	Arg	Ser	Asn	Glu	Thr
					35			40					45		
Val	Glu	Phe	Glu	Gly	Glu	Thr	Tyr	Pro	Leu	Ile	Arg	Val	Glu	Ile	Ser
					50			55				60			
Ser	Asp	Ser	His	Pro	Phe	Tyr	Thr	Gly	Arg	Gln	Lys	Phe	Thr	Gln	Ala
					65			70			75			80	
Asp	Gly	Arg	Val	Asp	Arg	Phe	Asn	Lys	Lys	Tyr	Gly	Leu	Lys		
					85				90						

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

Met	Glu	Thr	Ala	Leu	Ile	Ser	Val	Ile	Val	Pro	Val	Tyr	Asn	Val	Ala
1					5				10					15	
Gln	Tyr	Leu	Glu	Lys	Ser	Ile	Ala	Ser	Ile	Gln	Lys	Gln	Thr	Tyr	Gln
						20			25				30		
Asn	Leu	Glu	Ile	Ile	Leu	Val	Asp	Asp	Gly	Ala	Thr	Asp	Glu	Ser	Gly
						35			40			45			
Arg	Leu	Cys	Asp	Ser	Ile	Ala	Glu	Gln	Asp	Asp	Arg	Val	Ser	Val	Leu
					50			55			60				

His	Lys	Lys	Asn	Glu	Gly	Leu	Ser	Gln	Ala	Arg	Asn	Asp	Gly	Met	Lys
65						70				75					80
Pro	Gly	Ser	Arg	Gly	Leu	Ser	Asp	Phe	Tyr						
						85				90					

(2) INFORMATION FOR SEQ ID NO:434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

Met	Tyr	Phe	Leu	Ile	Asn	Phe	Val	Tyr	Pro	Val	Asp	Met	Val	Ile	Asn
1										10					15
Leu	Pro	Phe	Leu	Ile	Asn	Thr	Gly	Leu	Ile	Val	Leu	Leu	Ser	Ala	Ile
										25					30
Ser	Tyr	Ile	Ser	Leu	Leu	Val	Phe	Thr	Lys	Asp	Ser	Ile	Phe	Tyr	Glu
									35	40				45	
Phe	Leu	Asn	His	Val	Leu	Ala	Leu	Lys	Asn	Lys	Phe	Lys	Lys	Ser	
									50	55				60	

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

Met	Arg	Val	Ile	Ala	Trp	Leu	Glu	Pro	Ser	Arg	Lys	Ile	Leu	Gln	Pro
1															15
Gly	Ala	Asn	Asp	Val	Trp	Val	Val	Lys	Arg	Lys	Gly	Lys	Arg	Asp	Leu
															30
Leu	Leu	Pro	Tyr	Ile	Pro	Pro	Val	Val	Leu	Asn	Val	Asp	Ile	Pro	Asn
									35	40				45	

Lys Arg Val Asp Val Glu Ile Leu Glu Gly Leu Asp Asp Glu Asp
50 55 60

(2) INFORMATION FOR SEQ ID NO:436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

Met Asp Asp Asp Phe Lys Arg Tyr Asn Ala Pro Ile Leu Thr Trp Tyr
1 5 10 15
Glu Thr Ala Arg Tyr Ala Phe Glu Arg Gly Met Val Trp Gln Asn Leu
20 25 30
Gly Gly Val Glu Asn Ser Leu Asn Gly Gly Leu Tyr His Phe Lys Glu
35 40 45
Lys Phe Asn Pro Thr Ile Glu Glu Tyr Leu Gly Glu Phe Thr Met Pro
50 55 60
Thr His Pro Leu Tyr Pro Leu Leu Arg Leu Ala Leu Asp Phe Arg Lys
65 70 75 80
Thr Leu Arg Lys Lys His Arg Lys
85

(2) INFORMATION FOR SEQ ID NO:437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

Met Glu Asp Phe Phe Ala Trp Cys Arg Arg Gln Ser Val Leu Ser Gly
1 5 10 15
Ser Lys Leu Gly Arg Ala Ile Glu Tyr Ser Leu Lys Tyr Glu Glu Thr
20 25 30

Phe Lys Thr Ile Leu Lys Asp Gly His Leu Val Leu Ser Asn Asn Leu
35 40 45
Ala Glu Arg Ala Ile Lys Ser Leu Val Met Gly Arg Ser Lys Arg Val
50 55 60
Gln Trp Thr Leu Leu Ala
65 70

(2) INFORMATION FOR SEQ ID NO:438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

Met Thr Lys Gln Gly Ser Trp Lys Leu Ile Leu Glu Asp Glu Ser Ala
1 5 10 15
Gly Arg Glu Leu Phe Pro Ile Leu Thr Gln Gly Xaa Tyr Ile Ala Thr
20 25 30
Phe Asp Gln Gln Ala Pro Xaa Ile Asp Glu Ile Phe Lys Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

Met Thr Thr Asn Xaa Asp Asn Asp Thr Ser Glu Arg Ser Asp Cys Tyr
1 5 10 15
Arg Lys Arg Thr Ala Gly Glu Thr Pro Met Asn Asp Leu Thr Ser His
20 25 30
Thr His Gly Gly Asn Tyr Thr Ile Ala Arg Tyr Gln Glu Glu Lys Phe
35 40 45

Trp Asn Lys Gln Leu

50

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

Met	Ala	Gln	His	Ala	Ala	Val	Glu	Ala	Leu	Thr	Ala	Gly	Lys	Asn	Asp
1						5				10				15	
Ala	Glu	Pro	Met	Lys	Lys	Glu	Tyr	Ile	Gln	Arg	Arg	Asp	Tyr	Ile	Ile
			20					25					30		
Glu	Lys	Met	Thr	Ala	Leu	Gly	Phe	Glu	Ile	Ile	Lys	Pro	Asp	Gly	Ala
		35					40				45				
Phe	Tyr	Ile	Phe	Ala	Lys	Ile	Pro	Ala	Gly	Tyr	Asn	Gln	Asp	Ser	Phe
		50				55				60					
Ala	Phe	Leu	Lys	Asp	Phe	Ala	Gln	Lys	Lys	Ala	Val	Ala	Phe	Ile	Pro
	65				70				75				80		
Gly	Ala	Ala	Phe	Gly	Arg	Tyr	Gly	Glu	Gly	Tyr	Val	Arg	Leu	Ser	Tyr
			85				90				95				
Ala	Ala	Ser	Met	Glu	Thr	Ile	Lys	Glu	Ala	Met	Lys	Arg	Leu	Glu	Glu
			100					105				110			
Tyr	Met	Arg	Glu	Ala											
			115												

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

Met Asn Ile Thr Asn Leu Phe Ser Ile Lys Thr Gly Cys Asp Glu Thr
1 5 10 15
Asp Arg Gln Leu Gln Lys Leu Phe Phe Gln Leu Asp Leu Gln Leu Gly
20 25 30
Glu Leu Thr Asp Gln Leu Arg Lys Leu Asp Ser Asn Phe Val Pro Arg
35 40 45
Ser Gln Phe Val Asp Thr Leu Asp Leu Asn Asp Val Glu Tyr Lys Glu
50 55 60
Ile Leu Asn Tyr Phe Ile Phe His Arg Asn Asp Ser Glu Glu Ser Leu
65 70 75 80
Val Glu Trp Leu Tyr Asp Trp Ile Ser Thr Asn Arg Tyr Glu Leu Pro
85 90 95

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

Met Leu Gln Trp Ile Asp Arg Thr Phe Gln Asp Tyr Leu Glu Leu Glu
1 5 10 15
His Leu Val Leu Thr Thr Trp Ser Gly Asn Leu Gly Met Met Lys Leu
20 25 30
Ala Glu Lys Leu Xaa Met Lys Lys Xaa Ala His Ile Xaa Lys Val Arg
35 40 45
Tyr Tyr Gln Gly Lys Tyr Phe Asp Ser Ile Lys Tyr Gly Ile Leu Arg
50 55 60
Xaa Asp Trp Glu Lys Ile Asn Asp Gly Tyr Tyr Gln Ile Tyr Xaa Asn
65 70 75 80
Ser

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

Met Ile Val Glu Glu Val Arg Asp Arg Tyr Val Gly Lys Val Asp Ala
1 5 10 15
Val Phe His Asn Gly Asp Ser Glu Leu Arg Pro Asp Ser Pro Leu Trp
20 25 30
Glu Gly Ile Arg Val Val Lys Gly Asn Met Asp Phe Tyr Ala Gly Tyr
35 40 45
Pro Glu Arg Leu Val Thr Glu Leu Gly Ser Thr Lys Ile Ile Gln Thr
50 55 60
His Gly His Leu Phe Asp Ile Asn Phe Asn Phe Gln Lys Leu Asp Tyr
65 70 75 80
Trp Ala Gln Glu Glu Ala Ala Ile Cys Leu Tyr Gly His Leu His
85 90 95
Val Pro Ser Ala Trp Leu Glu Gly Lys Ile Leu Phe Leu Asn Pro Gly
100 105 110
Ser Ile Ser Gln Pro Arg Gly Thr Ile Arg Glu Cys Leu Tyr Ala Arg
115 120 125
Val Glu Ile Asp Asp Ser Tyr Phe Lys Val Asp Phe Leu Thr Arg Asp
130 135 140
His Glu Val Tyr Pro Gly Cys Pro Arg Ser Leu Ala Asp Asp Ala Lys
145 150 155 160
Glu Leu Arg Leu Ser Val Gly Ala Glu Asn Phe
165 170

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

Met Asn Leu His Gln Pro Leu His Val Leu Pro Gly Val Gly Pro Lys
1 5 10 15

Ser Ala Glu Lys Tyr Ala Lys Leu Gly Ile Glu Asn Leu Gln Asp Leu
 20 25 30
 Leu Leu Tyr Phe Pro Phe Arg Tyr Glu Asp Phe Lys Thr Lys Gln Val
 35 40 45
 Leu Glu Leu Glu Asp Gly Glu Lys Ala Val Leu Ser Gly Gln Val Val
 50 55 60
 Thr Pro Ala Ser Val Gln Tyr Tyr Gly Phe Gln Ala Ala Asn Pro Pro
 65 70 75 80
 Ala Phe Leu Val Leu Gln Ala Arg Glu Glu Gly Ser Phe Phe Phe Gly
 85 90 95
 Gly

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

Met Gln Leu Leu Ser Glu Asn Met Leu Lys Thr Ile Gln Ser Leu Ser
 1 5 10 15
 Val Trp Gln Ile Tyr Leu Leu Gly Phe Glu Arg Ile Leu Ala Leu Gly
 20 25 30
 Phe Gln Leu Leu Leu Thr Val Trp Val Tyr Gln Ala Val Arg Gln Lys
 35 40 45
 Lys Trp Ile Tyr Leu Leu Ala Ala Tyr Gly Leu His Ala Phe Phe Asp
 50 55 60
 Leu Ala Pro Ser Leu Phe Gln Val Gly Trp Leu Thr Asn Pro Val Leu
 65 70 75 80
 Val Glu Val Ile Leu Ala Leu Glu Leu Val Leu Val Ala Tyr Gly Thr
 85 90 95
 Lys Glu Ile Phe Cys Lys Lys Ser
 100

(2) INFORMATION FOR SEQ ID NO:446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

Met Thr Lys Ser Met Thr Pro Asp Arg Glu Val Ile Thr Phe Ile Pro
1 5 10 15
Glu Lys Phe Ile Val Asp Gly Phe Gln Gly Ile Arg Asp Pro Arg Gly
20 25 30
Met Met Gly Val Arg Leu Glu Met Arg Gly Leu Leu Tyr Thr Gly Pro
35 40 45
Arg Thr Ile Leu His Asn Leu Arg Lys Thr Val Glu Arg Ala Gly Val
50 55 60
Gln Val Glu Asn Val Ile Ile Ser Pro Leu Ala Met Val Gln Ser Val
65 70 75 80
Leu Asn Glu Gly Glu Arg Glu Phe Gly Ala Thr Val Ile Asp Met Gly
85 90 95
Ala Gly Gln Thr Thr Val Ala Thr Ile Arg Asn Gln Glu Leu Gln Phe
100 105 110
Thr His Ile Leu Gln Glu Val Glu Ile Met
115 120

(2) INFORMATION FOR SEQ ID NO:447:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 123 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

Met Leu Asn Ser Ile Val Thr Ile Ile Cys Ile Ala Leu Ile Ala Phe
1 5 10 15
Ile Leu Phe Trp Phe Phe Lys Lys Pro Glu Lys Ser Gly Gln Lys Ala
20 25 30
Gln Gln Lys Asn Gly Tyr Gln Glu Ile Arg Val Glu Val Met Gly Gly
35 40 45

Tyr Thr Pro Glu Leu Ile Val Leu Lys Lys Ser Val Pro Ala Arg Ile
50 55 60
Val Phe Asp Arg Lys Asp Pro Ser Pro Cys Leu Asp Gln Ile Val Phe
65 70 75 80
Pro Asp Phe Gly Val His Ala Asn Leu Pro Met Gly Glu Glu Tyr Val
85 90 95
Val Glu Ile Thr Pro Glu Gln Ala Gly Glu Phe Gly Phe Ala Cys Gly
100 105 110
Met Asn Met Met His Gly Lys Met Ile Val Glu
115 120

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

Met Lys Ile Val Ser Gly Ile Tyr Gly Gly Arg Pro Leu Lys Thr Leu
1 5 10 15
Glu Gly Lys Thr Thr Arg Pro Thr Ser Asp Lys Val Arg Gly Ala Ile
20 25 30
Phe Asn Met Ile Gly Pro Tyr Phe Glu Val Gly Xaa Val Leu Asp Leu
35 40 45
Tyr Ala Gly Ser Gly Gly Leu Ser Ile Glu Ala Val Ser Arg Gly Met
50 55 60
Ser Ser Ala Val Leu Val Glu Arg Asp Arg Lys Ala Gln Thr Ile Val
65 70 75 80
Ala Glu Asn Ile Gln Met Thr Lys Glu Val Gly Lys Phe Gln Leu Leu
85 90 95
Gln Asn Gly Cys Arg Lys Gly Ile Gly Thr Gly Xaa Leu Gly Asn Leu
100 105 110
Thr Ser Phe Ser
115

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

Met Xaa Thr Asn Phe Thr Asp Gln Val Asp Thr Met Ile Tyr Val Asp
1 5 10 15
Lys Glu Glu Lys Glu Thr Ile Lys Ala Ala Leu Val Glu Phe Phe Asn
20 25 30
Gly Lys Val Thr Leu Thr Asp Gln Gly Leu Arg Glu Val Glu Val Pro
35 40 45
Val Asn Leu Val
50

(2) INFORMATION FOR SEQ ID NO:450:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 75 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

Met Ile Gly Val Ala Leu Glu Glu Ser Pro Thr Leu Lys Ile His His
1 5 10 15
Leu Thr His Asp Ile Thr Pro Tyr Asn Ile Phe Glu Gly Ser Tyr Arg
20 25 30
Leu Phe Gln Thr Val Asp Tyr Trp Pro Glu Gly Thr Thr Phe Val Ser
35 40 45
Val Val Asp Pro Gly Val Gly Ser Lys Arg Lys Ser Val Val Ala Lys
50 55 60
Thr Ala Gln Lys Ser Ile His Cys His Ala Arg
65 70 75

(2) INFORMATION FOR SEQ ID NO:451:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 130 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

Met Glu Leu Arg Arg Pro Arg Leu Ala Asp Lys Lys Ala Val Leu Asp
1 5 10 15
Met Met Thr Glu Phe Glu Lys Ser Gln Ser Ala His Asp Gly Gly Phe
20 25 30
Trp Asp Thr Glu Asn Phe Val Tyr Glu Glu Trp Leu Glu Ser Asn Gln
35 40 45
Glu Gln Glu Met Gly Ile Asn Leu Pro Glu Gly Trp Val Pro Ala Ile
50 55 60
Gln Leu Val Ala Phe Ser Glu Lys Gly Gln Ala Val Gly Phe Leu Asn
65 70 75 80
Leu Arg Leu Arg Leu Ser Asn Phe Leu Leu Glu Glu Gly His Ile
85 90 95
Gly Tyr Ser Ile Arg Pro Ser Glu Arg Gly Lys Gly Tyr Ala Lys Glu
100 105 110
Leu Ser Val Arg Ala Cys Lys Leu Leu Arg Lys Arg Thr Ser Arg Lys
115 120 125
Leu Trp
130

(2) INFORMATION FOR SEQ ID NO:452:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 63 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

Met Thr Phe Ile Arg Gly Pro Ile Ile Ser Thr Val Gly Glu Gly Val
1 5 10 15
Xaa Ile Leu Ala Thr Val Asn Xaa Gln Phe Val Xaa Xaa Gln Xaa Xaa
20 25 30

Asn Met Leu Val Ser Pro Phe His Pro Glu Leu Thr Asp Xaa Xaa Arg
35 40 45
Leu Xaa Gln Tyr Phe Ile Ser Met Cys Lys Glu Lys Ser Xaa Asp
50 55 60

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

Met Lys Gly Asp Val Ile Thr Glu His Gln Phe Tyr Glu Gln Val Lys
1 5 10 15
Asn Asn Pro Ser Ala Gln Xaa Val Leu Leu Asn Met Thr Ile Gln Lys
20 25 30
Val Phe Glu Lys Thr Ile Trp Leu Arg Ala
35 40

(2) INFORMATION FOR SEQ ID NO:454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

Met Asp Lys Ala Leu Ala Asp Leu Lys Thr Ser Gly His Leu Pro Ile
1 5 10 15
Pro Arg His Leu Arg Asp Gly His Tyr Xaa Gly Ser Lys Glu Leu Gly
20 25 30
Asn Ala Gln Asp Tyr Leu Tyr Pro His Asn Tyr Pro Xaa Asn Trp Val
35 40 45
Lys Gln Asp Tyr Leu Pro Gln Lys Ile Arg Asn His His Tyr Phe Gln
50 55 60

Ala Glu Tyr Thr Gly Lys Tyr Glu Arg Ala Leu Ala Gln Arg Lys Glu
65 70 75 80
Ala Ile Asp His Leu Arg Lys Ile
85

(2) INFORMATION FOR SEQ ID NO:455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

Met Val Val Phe Thr Gly Ser Thr Val Glu Glu Ala Ile Gln Lys Gly
1 5 10 15
Leu Lys Glu Leu Asp Ile Pro Arg Met Lys Ala His Ile Lys Val Ile
20 25 30
Ser Arg Glu Lys Lys Gly Phe Leu Gly Leu Phe Gly Lys Lys Pro Ala
35 40 45
Gln Val Asp Ile Glu Ala Ile Ser Glu Thr Thr Val Val Lys Ala Asn
50 55 60
Gln Gln Val Val Lys Gly Val Pro Lys Lys Ile Asn Asp Leu Asn Glu
65 70 75 80
Pro Val Lys Thr Val Ser Val Arg Asn Arg
85 90

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

Met Thr Lys Arg Cys Ser Trp Val Lys Met Thr Asn Pro Leu Tyr Ile
1 5 10 15

Ala Tyr His Asp Glu Glu Trp Gly Gln Pro Leu His Asp Asp Gln Ala
20 25 30
Leu Phe Glu Leu Leu Cys Met Glu Thr Tyr Gln Ala Gly Leu Ser Trp
35 40 45
Glu Thr Val Leu Asn Lys Arg Gln Ala Phe Arg Glu Ala Phe Pro
50 55 60

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

Met Phe Val Gly Gln Glu Trp Thr Asn Gln Thr Phe Val Asp Leu Leu
1 5 10 15
Gly Asn His Gln Gly Gln Val Thr Ile Asp Glu Glu Gly Tyr Gly Gln
20 25 30
Phe Pro Val Ser Ala Arg Ser Val Ser Val Trp Ala Val Asn Thr Ile
35 40 45

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

Met Ala Gln Val Asp Ile Ile His Gly Ile Gly Thr Gly Val Ile Arg
1 5 10 15
Glu Gly Val Thr Lys Tyr Leu Gln Arg Asn Lys His Val Lys Ser Phe
20 25 30
Gly Tyr Ala Pro Gln Asn Ala Gly Gly Ser Gly Ala Thr Ile Val Thr
35 40 45

Phe Lys Gly

50

(2) INFORMATION FOR SEQ ID NO:459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

Met	Asn	Leu	Leu	Glu	Glu	Ala	Thr	Lys	Gly	Lys	Val	Ile	Phe	Glu	Gly
1				5							10				15
Val	Asp	Ile	Thr	Asp	Lys	Lys	Asn	Asp	Leu	Phe	Pro	Met	Arg	Glu	Lys
					20				25					30	
Met	Gly	Met	Val	Phe	Gln	Gln	Phe	Asn	Xaa	Phe	Leu	Ile			
				35				40					45		

(2) INFORMATION FOR SEQ ID NO:460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

Met	Gln	Ile	Asp	Leu	Ala	Asn	Leu	Leu	Pro	Asp	Leu	Pro	Gly	Asn	Leu
1				5					10					15	
Ser	Gly	Ile	Asn	Pro	Asn	Arg	Tyr	Val	Phe	Tyr	Gln	Asp	Val	Leu	Cys
					20			25					30		
Pro	Ile	Leu	Asp	Arg	His	Met	Thr	Pro	Glu	Gln	Asp	Lys	Pro	His	Phe
					35			40				45			
Ala	Gln	Ala	Ala	Gly	Thr	Ile	Ala	Asp	Ile	Lys	Glu	Lys	Ala	Gly	Asn
				50				55			60				
Tyr	Ala	Tyr	Leu	Phe	Glu	Thr	Gln	Ala	Gln	Leu	Asn	Ala	Ile	Leu	Ser
				65				70			75			80	

Ser Lys Val Asp Val Gly Arg Arg Ile Arg His Ala Tyr Gln Ala Asp
85 90 95
Asp Lys Glu Ser Leu Gln Gln Ile Ala Arg Gln Glu Leu Pro Glu Leu
100 105 110
Arg Ser Gln Ile Glu Asp Phe His Ala Leu Phe Ser His His Trp Leu
115 120 125
Lys

(2) INFORMATION FOR SEQ ID NO:461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

Met Arg Gln Gly Ile Asp Ser Leu Ala Tyr Val Val Lys Thr His Phe
1 5 10 15
Glu Leu Asp Pro Phe Ser Gly Gln Ala Phe Leu Phe Cys Gly Gly Arg
20 25 30
Lys Asp Arg Phe Lys Ala Leu Tyr Trp Asp Gly Gln Gly Phe Trp Leu
35 40 45
Leu Tyr Lys Arg Phe Glu Asn Gly Lys Leu Thr
50 55

(2) INFORMATION FOR SEQ ID NO:462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

Met Asn Ala Phe Leu Glu Glu Leu Ser Gln Ala Tyr Pro Asp Asp Tyr
1 5 10 15

Phe	Leu	Leu	Val	Met	Asp	Asn	Ala	Ile	Trp	His	Lys	Ser	Ser	Val	Leu
				20					25					30	
Lys	Ile	Pro	Thr	Asn	Ile	Gly	Phe	Ala	Phe	Ile	Pro	Pro	Tyr	Thr	Pro
				35					40				45		
Glu	Met	Asn	Pro	Ile	Glu	Gln	Val	Trp	Lys	Glu	Ile	Arg	Lys	Arg	Gly
	50					55				60					
Phe	Lys	Asn	Lys	Ala	Phe	Arg	Ile	Leu	Glu	Asp	Val	Met	Asn	Gln	Leu
65					70				75				80		
Gln	Asp	Val	Ile	Gln	Gly	Leu	Glu	Lys	Glu	Val	Ile	Lys	Ser	Ile	Val
						85			90				95		
Asn	Arg	Arg	Trp	Thr	Arg	Met	Leu	Phe	Glu	Ser	Arg				
						100			105						

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

Met	Thr	Val	Glu	Glu	Glu	Lys	Val	Phe	Leu	Ala	Arg	His	Leu	Lys	Ala
1					5				10				15		
Thr	Glu	Ala	Gly	Glu	Phe	Val	Thr	Ile	Asp	Ala	Leu	Phe	Gln	Ala	Tyr
					20				25				30		
Lys	Lys	Glu	Leu	Gly	Arg	Ser	Tyr	Thr	Arg	Asp	Ala	Phe	Tyr	Gln	Leu
					35				40				45		
Leu	Lys	Arg	His	Gly	Trp	Arg	Asn	Ile	Met	Pro	Arg	Pro	Glu	His	Pro
					50				55				60		
Lys	Lys	Ala	Asp	Ala	Gln	Thr	Ile	Val	Ala	Ser	Lys	Asn	Lys	Ile	Ser
65						70				75			80		
Ile	Gln	Glu	Asp	Lys	Lys	Ala	Ile								
					85										

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

Met	Leu	Ser	Leu	Val	Val	Leu	Ile	Thr	Gln	Tyr	Ala	Thr	His	Gly	Glu
1									10						15
Leu	Phe	Glu	Asn	Tyr	Ile	Ser	Lys	Glu	Asn	Asp	Asn	Val	Ile	Lys	Glu
	20							25						30	
Tyr	Gln	Asn	Thr	Thr	Gly	Phe	Ser	Thr	Pro	Tyr	Thr	Leu	Asp	Gly	Ser
	35						40						45		
Val	Leu	Ile	Val	His	Pro	Asp	Leu	Thr	Lys	Gly	Met	Asn	Ile	Glu	Gly
	50					55				60					
Tyr	Ser	Asp	Leu	Leu	Lys	Pro	Glu	Leu	Lys	Gly	Lys	Ile	Ala	Thr	Ala
	65					70			75					80	
Asp	Pro	Ala	Asn	Ser	Ser	Ala	Phe	Ala	Gln	Leu	Thr	Asn	Met	Leu	
							85		90				95		
Gln	Ala	Gln	Gly	Gly	Tyr	Lys	Asp	Asp	Leu	Ala	Trp	Ser	Val	Leu	Ser
					100			105					110		
Thr	Ile	Phe	Ser	Thr	Leu	Ile	Asp	Gly	Ile	Val	Lys				
						115			120						

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

Met	Leu	Ala	Arg	Lys	Asp	Arg	Phe	Tyr	Tyr	Ile	Asp	Lys	Ala	Thr	Gly
1							5			10				15	
Lys	Ala	Leu	Gly	Ile	Phe	Leu	Ser	Cys	Val	Leu	Thr	Ser	Asn	Gly	Val
							20			25				30	
Ile	Glu	Val	Gly	Ala	Val	Thr	Phe	Ser	Pro	Lys	Leu	Arg	Gly	Thr	Arg
							35		40				45		

Ile Gly Thr Glu Ala Gln Tyr Leu Leu Ala Arg Tyr Val Phe Glu Glu
50 55 60
Leu Asn Tyr Arg Arg Tyr Glu Trp Lys Cys Asp Ala Leu Asn Leu Pro
65 70 75 80
Ser Arg Arg Ala Ala Glu Arg Leu Gly Phe Ile Tyr Glu Gly Thr Phe
85 90 95
Arg Gln Ala Val Val Tyr Lys Gly Arg Thr Arg Asp Met Asp Trp Leu
100 105 110
Ser Met Ile Asp Lys Asp Trp Pro Lys Val Lys Asp Arg Leu Glu Thr
115 120 125
Trp Leu Arg Pro Glu Asn Phe Asp Lys Asn Gly Gln Gln Tyr Lys Ser
130 135 140
Leu Arg Glu Leu
145

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

Met Met Thr Ser Asp Phe Phe Glu Val Trp Phe Gln Lys Phe Leu Leu
1 5 10 15
Pro Thr Leu Thr Thr Pro Ser Val Ile Ile Val Lys
20 25

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

Met Val Ser Thr Lys Thr Gln Ile Ala Gly Phe Glu Phe Asp Asn Cys
1 5 10 15
Leu Met Asn Ala Ala Gly Val Ala Cys Met Thr Ile Glu Glu Leu Glu
20 25 30
Glu Val Lys Asn Ser Ala Ala Gly Thr Phe Val Thr Lys Thr Ala Thr
35 40 45
Leu Asp Phe Arg Gln Gly Asn Pro Glu Pro Arg Tyr Gln Asp Val Pro
50 55 60
Leu Gly Ser Ile Asn Ser Met Gly Leu Pro Asn Asn Gly Leu Asp Tyr
65 70 75 80
Tyr Leu Asp Tyr Leu Leu Asp Leu Gln Glu Lys Glu Ser Asn Arg Thr
85 90 95
Phe Phe Leu Ser Leu Val Gly Met Ser Pro Glu Lys Pro Ile Leu Phe
100 105 110

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

Met Thr Tyr Leu Met Phe Ser Gly Leu Asp Glu Asn Phe Tyr His Phe
1 5 10 15
Pro Trp Glu Val Phe Ala Gly Phe Gly Ile Ile Phe Leu Ala Cys Pro
20 25 30
Glu Lys Val
35

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

Met Phe Thr Gly Trp Phe Ala Gln Thr Phe Leu His Gln Phe Ile Arg
1 5 10 15
Gly Ala Trp Gly Leu Gly Phe Met Ile Phe Ile Ala Phe Pro Met Gly
20 25 30
Lys Glu Leu Leu Glu Gly Glu Tyr His Glu His Asp
35 40

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

Met Gln Glu Lys Ile Leu Val Thr Gly Gly Ala Gly Phe Ile Gly Thr
1 5 10 15
His Thr Val Ile Glu Leu Ile Gln Ala Gly His Gln Val Val Val Val
20 25 30
Asp Asn Leu Val Asn Ser Asn Xaa Lys Ser Leu Glu Val Val Glu Arg
35 40 45
Ile Thr Gly Val Glu Ile Pro Phe Tyr Glu Ala Asp Ile Xaa Asp Thr
50 55 60
Asp Thr Leu Arg Asp Ile Phe Lys Gln Glu Glu Leu Thr Gly Val Ile
65 70 75 80
His Phe Ala Gly Leu Lys Ala Val Gly Glu Ser Thr Arg Ile Pro Leu
85 90 95
Ala Tyr Tyr Asp Asn Asn Ile Ala Gly Thr Val Ser Leu Leu Lys Ala
100 105 110
Met Glu Glu Asn Asn Cys Lys Asn Ile Ile Phe Ser Ser Xaa Ala Thr
115 120 125
Val Tyr Gly Asp Pro Tyr Thr Val Pro Ile Leu Glu Val Ser His Phe
130 135 140
Gln
145

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

Met	Val	Lys	Glu	Lys	Val	Thr	Leu	Thr	Pro	Leu	Ala	Ser	Gly	Tyr	Gln
1					5				10						15
Ile	Gly	Glu	Glu	Glu	Phe	Glu	Gln	Val	Ile	Leu	Ala	Xaa	Gly	Ala	Trp
	20							25							30
Leu	Gly	Asp	Met	Leu	Glu	Pro	Leu	Gly	Tyr	Glu	Val	Asp	Val	Arg	Pro
	35							40							45
Gln	Lys	Gly	Gln	Leu	Arg	Asp	Tyr	Gln	Leu	Val	Gln	Asp	Met	Glu	Ala
	50							55							60
Tyr	Pro	Val	Val	Met	Pro	Glu	Gly	Glu	Trp	Asp	Leu	Ile	Pro	Phe	Ala
	65					70				75					80
Gly	Gly	Lys	Leu	Ser	Leu	Gly	Ala	Thr	His	Glu	Asn	Asp	Met	Gly	Phe
	85							90							95
Asp	Leu	Thr	Val	Asp	Glu	Thr	Leu	Leu	Gln	Met	Glu	Glu	Ala	Thr	
			100						105						110
Leu	Thr	His	Tyr	Leu	Ile	Leu	Ala	Glu	Ala	Thr	Ser	Lys	Ser	Glu	Arg
	115							120				125			
Val	Gly	Ile	Arg	Ala	Tyr	Thr	Ser	Asp	Phe	Ser	Pro	Phe	Phe	Gly	Gln
	130							135							140
Val	Pro	Asp	Leu	Thr	Gly	Val	Tyr	Ala	Ala	Ser	Gly	Leu	Gly	Ser	Ser
	145							150			155				160
Gly	Leu	Thr	Thr	Gly	Pro	Ile	Ile	Gly	Tyr	His	Leu	Ala	Gln	Leu	Ile
						165				170					175
Gln	Asp	Lys	Glu	Leu	Thr	Leu	Asp	Pro	Glu	Asn	Tyr	Pro	Ile	Glu	Asn
						180			185						190
Tyr	Val	Lys	Arg	Val	Lys	Ser	Glu								
					195				200						

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

Met Glu His Ile Ile Tyr Gln Phe Glu Glu Asp Leu Ala Ile Leu Thr
1 5 10 15
Leu Asn Arg Pro Glu Val Ala Asn Gly Phe His Ile Pro Met Cys Glu
20 25 30
Glu Ile Leu Glu Ala Leu Thr Leu Ala Glu Glu Asn Pro Ala Val His
35 40 45
Phe Ile Leu Ile Asn Ala Asn Gly Lys Val Phe Ser Val Gly Gly Asp
50 55 60
Leu Val Glu Met Lys Arg Ala Val Asp Glu Asp Asp Ile Pro Ser Leu
65 70 75 80
Thr Lys Ile Ala Glu Leu Val Asn Thr Ile Ser Tyr Lys Ile Lys Gln
85 90 95
Ile Ala Lys Pro Val Phe Asn Gly Ser
100 105

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

Met Gln Pro Glu Val Ile Trp Leu Gln Lys Ile Ala Lys Pro Ser Gln
1 5 10 15
Met Lys Val Leu Asn Thr Thr Asp Arg Val Gln Ala Ile Lys Asp Asp
20 25 30
Val Asp Ile Ile Gln Asn Ser Leu Gln Ile Ile Asn Gln Gln Lys Glu
35 40 45
Leu Ile Lys Glu Tyr Gln Glu Asp Leu Thr Tyr Lys Phe Lys Val Leu
50 55 60
Glu Lys Asp Ile Gln Thr Arg Thr Ser Cys Asp Lys Arg Asn Ala Gly
65 70 75 80
Asn

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

Met Gly Ser Asn Ser Leu Thr Leu Leu Lys Ile Gln Ala Thr Ile
1 5 10 15
Pro Arg Asn Ile Tyr Asp Asn Leu Gln Ala Gly Ser Lys Val Thr Leu
20 25 30
Asp Arg Ala Tyr Gly His Met Ile Ile Glu Glu Gly Arg Glu Asn Gln
35 40 45
Val Trp Ile Ala Gly Gly Ile Gly Ile Thr Pro Phe Ile Ser Tyr Ile
50 55 60
Arg Glu His Pro Ile Leu Asp Lys Gln Val His Phe Tyr Tyr Ser Phe
65 70 75 80
Arg Gly Asp Glu Asn Ala Val Tyr Leu Asp Leu Leu Arg Asn Tyr Ala
85 90 95
Gln Lys Asn Pro Asn Phe Glu Leu His Leu Ile Asp Ser Thr Lys Asp
100 105 110
Gly Tyr Leu Asn Phe Glu Gln Lys Lys Cys Pro Asn Met Gln Pro Ser
115 120 125
Ile Cys Val Val Leu Phe Leu
130 135

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

Met Phe Phe Val Leu Ala Tyr Ala Lys Ala Val Ala Gly Arg Asn Ile
 1 5 10 15
 Lys Leu His Pro Ile Gln Arg Gln Gly Ala Gly Tyr His Ser Val Asn
 20 25 30
 Lys Asp Val Asp Phe Ala Ser Ala Thr Ala Leu Arg Gln His Gln Lys
 35 40 45
 Asp Gln Asp Phe Leu Glu Arg Phe Met Pro Ser Val Ala Leu Phe Glu
 50 55 60
 Gln Ala Ser Lys Val Ile Trp Glu Asp Tyr Phe Pro Leu Leu Arg Tyr
 65 70 75 80
 Gln Ile Leu Ser Asn Pro Asp Leu Thr Thr Ile Tyr Gln Val Asn Gln
 85 90 95
 Glu Met Ala Val Arg Ile Lys Glu Ala Ile Lys Thr Ala Gln Ser Val
 100 105 110
 Glu Glu Leu Val Glu Leu Val Thr Thr Lys Arg Tyr Thr Lys Ala Arg
 115 120 125
 Val Arg Arg Leu Leu Thr Tyr Ile Leu Met Gln Ala Arg Glu Ser Asp
 130 135 140
 Leu Pro Glu Ala Ile His Val Leu Gly Phe Thr Glu Lys Gly Arg Gln
 145 150 155 160
 His Leu Lys Ser Leu Lys Gly Gln Val Asn Leu Val Ser Arg Ile Gly
 165 170 175
 Lys Glu Pro Trp Asp Ala Met Thr Gln Lys Val Asp Gln Ile Tyr Gln
 180 185 190
 Leu Gly Lys Pro Ser Ile Ala Glu Gln Asn Phe Gly Arg Val Pro Ile
 195 200 205
 Arg Ile Glu Thr Asn
 210

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

Met Leu Gly Ser Met Phe Val Gly Leu Leu Val Gly Phe Leu Ala Gly
 1 5 10 15

Ala Met Thr Asn Arg Gly Glu Arg Met Gly Cys Phe Gly Lys Met Phe
20 25 30
Leu Gly Trp Ile Gly Ala Phe Leu Gly His Leu Leu Phe Gly Thr Trp
35 40 45
Gly Pro Val Leu Ser Gly Thr Ala Ile Ile Pro Ala Val Leu Gly Ala
50 55 60
Met Ile Val Leu Ala Ile Phe Trp Arg Arg Gly Ser
65 70 75

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

Met Arg Ser Ser Pro Ser Arg Glu Ile Gln Pro Arg Ser Trp Gly Ile
1 5 10 15
Thr Thr Val Tyr Val Thr His Asp Gln Glu Gly Ala Met Ala Ile Ser
20 25 30
Asp Gln Ile Ala Cys Tyr Glu Arg Trp Gly Asp Pro Thr Asn Arg Pro
35 40 45
Thr Lys Arg Thr Val Ser
50

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a polynucleotide sequence selected from the group consisting of:
 - 5 (a) a polynucleotide having at least a 70% identity to a polynucleotide encoding a polypeptide comprising an amino acid sequence of selected from the group consisting of SEQ ID NO:224 through 477,
 - (b) a polynucleotide which is complementary to the polynucleotide of (a);
 - (c) a polynucleotide having at least a 70% identity to a polynucleotide encoding the
 - 10 same mature polypeptide expressed by the gene comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1 through 223 contained in the DNA of the deposited clone; and
 - (d) a polynucleotide comprising at least 15 sequential bases of the polynucleotide of (a), (b) or (c).
- 15 2. The polynucleotide of Claim 1 wherein the polynucleotide is DNA.
3. The polynucleotide of Claim 1 wherein the polynucleotide is RNA.
4. The polynucleotide of Claim 2 comprising the nucleic acid sequence set forth in SEQ ID NO:1.
5. The polynucleotide of Claim 2 comprising a nucleotide sequence selected from
- 20 the group consisting of SEQ ID NO:1 through 223.
6. The polynucleotide of Claim 2 which encodes a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:224 through 477.
7. A vector comprising the polynucleotide of Claim 1.
8. A host cell comprising the vector of Claim 7.
- 25 9. A process for producing a polypeptide comprising: expressing from the host cell of Claim 8 a polypeptide encoded by said DNA.
10. A process for producing a novel polypeptide or fragment comprising culturing a host of claim 8 under conditions sufficient for the production of said polypeptide or fragment.
- 30 11. A polypeptide comprising an amino acid sequence which is at least 70% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:224 through 477.
12. A polypeptide comprising an amino acid selected from the group consisting of SEQ ID NO:224 through 477.

13. An antibody against the polypeptide of claim 11.
14. An antagonist which inhibits the activity or expression of the polypeptide of claim 11.
15. A method for the treatment of an individual in need of a Streptococcal polypeptide comprising: administering to the individual a therapeutically effective amount of the polypeptide of claim 11.
- 5 16. A method for the treatment of an individual having need to inhibit a bacterial polypeptide comprising: administering to the individual a therapeutically effective amount of the antagonist of Claim 14.
- 10 17. A process for diagnosing a disease related to expression or activity of the polypeptide of claim 11 in an individual comprising:
 - (a) determining a nucleic acid sequence encoding said polypeptide, and/or
 - (b) analyzing for the presence or amount of said polypeptide in a sample derived from the individual.
- 15 18. A method for identifying compounds which interact with and inhibit or activate an activity of the polypeptide of claim 11 comprising:

contacting a composition comprising the polypeptide with the compound to be screened under conditions to permit interaction between the compound and the polypeptide to assess the interaction of a compound, such interaction being associated with a second component capable of

20 providing a detectable signal in response to the interaction of the polypeptide with the compound;

and determining whether the compound interacts with and activates or inhibits an activity of the polypeptide by detecting the presence or absence of a signal generated from the interaction of the compound with the polypeptide.
- 25 19. A method for inducing an immunological response in a mammal which comprises inoculating the mammal with Streptococcal polypeptide of claim 11, or a fragment or variant thereof, adequate to produce antibody and/or T cell immune response to protect said animal from disease.
- 30 20. A method of inducing immunological response in a mammal which comprises delivering a nucleic acid vector to direct expression of Streptococcal polypeptide of claim 11, or fragment or a variant thereof, for expressing said Streptococcal polypeptide, or a fragment or a variant thereof *in vivo* in order to induce an immunological response to produce antibody and/ or T cell immune response to protect said animal from disease.

21. An isolated Streptococcal polypeptide having one of the amino acid sequences of SEQ ID NO:224 through SEQ ID NO:234.
22. An isolated nucleic acid encoding one of the amino acid sequences of Claim 21 and nucleic acid sequences capable of hybridizing therewith under stringent conditions.
23. Recombinant vectors comprising the nucleic acid sequences of Claim 22 and host cells transformed or transfected therewith.
24. A method of identifying an antimicrobial compound comprising contacting candidate compounds with a polypeptide of Claim 21 and selecting those compounds capable of inhibiting the bioactivity of said polypeptide.
25. Antimicrobial compounds identified by the method of Claim 24.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US97/05306

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :Please See Extra Sheet.

US CL :536/23.7; 435/6, 69.1, 252.3, 320.1; 530/324, 350; 514/12

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/23.7; 435/6, 69.1, 252.3, 320.1; 530/324, 350; 514/12

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Please See Extra Sheet.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X, P ---	WO 96/10647 A1 (FUSO PHARMACEUTICAL INDUSTRIES, LTD.) 11 April 1996, claim 2, pages 22-24.	1, 2, 7, 8, and 22 -----
Y, P		3, 6, 9-12, 15, 17, 21, and 23-25
Y	WATSON, J. D. et al. Recombinant DNA, Second Edition. New York: Scientific American Books, W.H. Freeman and Company, 1992, pages 73 and 74, see entire document.	1-3, 6-12, 15, 17, and 21-23
Y	KENNELL, D. E. Principles and Practices of Nucleic Acid Hybridization. Progress in Nucleic Acid Research Molecular Biology. 1971, Vol. 11, pages 259-301, see especially pages 259-262.	1-3, 6-12, 15, 17, and 21-23

Further documents are listed in the continuation of Box C. See patent family annex.

Special categories of cited documents:	T	later documents published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A document defining the general state of the art which is not considered to be of particular relevance	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
B earlier document published on or after the international filing date	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
L document which may throw doubt on priority claim(s) or which is cited to establish the publication date of another citation or other special reasons (as specified)		
O document referring to an oral disclosure, use, exhibition or other means	"E"	document member of the same patent family
P document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search

10 JULY 1997

Date of mailing of the international search report

06 AUG 1997

Name and mailing address of the ISA/US
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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/05306

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:

2. Claims Nos.: because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-3, 6-12, 15, 17, and 21-23 (SEQ ID NOS 224-233).

Remark on Protest

- The additional search fees were accompanied by the applicant's protest.
 No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORTInternational application No.
PCT/US97/05306**BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING (Continued):**

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I. Claims 1-12, 15, 17, and 21-23, drawn to nucleic acids and polypeptides of specific sequence, vectors containing nucleic acids, methods of producing polypeptides, and methods of treatment using polypeptides.

Group II. Claims 13 and 19, drawn to antibodies against any of no fewer than 254 specific sequence polypeptides.

Group III. Claims 14 and 16, drawn to antagonists of undisclosed composition of the activity of no fewer than 254 specific sequence polypeptides.

Group IV. Claims 18 and 24, drawn to methods for screening for compounds that interact with no fewer than 254 specific sequence polypeptides.

Group V. Claim 20, drawn to a method of inducing an immunological response using a nucleic acid.

Group VI. Claim 25, drawn to compounds of undisclosed composition.

The inventions listed as Groups I-VI do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons. The nucleic acids, proteins, and methods of Group I are materially different from the antibodies of Group II, the compounds of Group III, and the compounds of Group VI and are not required to produce either the antibodies of Group II, which antibodies may be made with antigens other than those embraced by Group I. Additionally, the methods of Group I are not needed to produce the compounds of either one of Groups III or VI. The compositions and methods of Group I are not needed for the methods of either one of Groups IV or V. The antibodies of Group II are not needed for the methods of Groups IV or V and are materially different from the compounds of Groups III and VI. The antagonists of Group III are materially different from the compounds of Group VI because the antagonists and compounds have differing sites of action and/or binding. Neither are the compounds of either one of Groups III or VI needed to practice the methods of either one of Groups IV or V. The methods of Groups IV and V may be practiced independently of one another.

This application contains claims directed to more than one species of the generic invention. These species are deemed to lack Unity of Invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be searched, the appropriate additional search fees must be paid. The species are as follows. Each of the 234 SEQ ID NOs listed is a separate species because there is no relationship between the species.

The species listed above do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, the species lack the same or corresponding special technical features for the following reasons. There is no relationship among the species.

For any Group applicant elects, a total of 10 (TEN) specified sequences will be searched and no more than 4 (FOUR) specified sequences will be searched for each additional fee paid.

The claims are deemed to correspond to the species listed above in the following manner: SEQ ID NOs 224-233 correspond to claims 1-3, 6-12, 15, 17, and 21-23.

A. CLASSIFICATION OF SUBJECT MATTER:

IPC (6):

C12N 15/31, 15/11, 15/00; C12P 21/02; A61K 38/16, 39/09; C07K 14/195, 14/315

B. FIELDS SEARCHED

Electronic data bases consulted (Name of data base and where practicable terms used):

MPSRCH OF: A-GENESEQ26, A-ISSUED, HIV-AA8, PIRSO, SUIWW-PROT34, EMBL-NEW11, GENBANK97, GENBANK-NEW11, U-EMBL48_97, HIV-NA8, N-GENESEQ26, N-ISSUED, EST-STS, EST-STS-TWO, EST-STS-

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/05306

THREE. SEQ ID NO: 224-233.